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P104185GB

2. Patent application number

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0328106.0

3. Full name, address and postcode of the or of each applicant (underline all surnames)

Ludwig Institute for Cancer Research
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Switzerland

Patents ADP number (if you know it)

577155002

If the applicant is a corporate body, give the country/state of its incorporation

CH

4. Title of the invention

Screening Assay

5. Name of your agent (if you have one)

Harrison Goddard Foote

"Address for service" in the United Kingdom to which all correspondence should be sent (including the postcode)

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Rob Docherty

01904 732120

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Screening Assay

The invention relates to an screening assay for the identification of agents which modulate the activity of polypeptides which affect the apoptotic activity of the 5 tumour suppressor protein p53.

Tumour suppressor genes encode proteins which function to inhibit cell growth or division and are therefore important with respect to maintaining proliferation, growth and differentiation of normal cells. Mutations in tumour suppressor genes result in 10 abnormal cell-cycle progression whereby the normal cell-cycle check points which arrest the cell-cycle, when, for example, DNA is damaged, are ignored and damaged cells divide uncontrollably. The products of tumour suppressor genes function in all parts of the cell (e.g. cell surface, cytoplasm, nucleus) to prevent the passage of damaged cells through the cell- cycle (i.e. G1, S, G2, M and cytokinesis). Arguably 15 the tumour suppressor gene which has been the subject of the most intense research is p53. p53 encodes a protein which functions as a transcription factor and is a key regulator of the cell division cycle. It was discovered as a protein shown to bind with affinity to the SV40 large T antigen. The p53 gene encodes a 393 amino acid polypeptide with a molecular weight of 53kDa.

20 We have described a family of proteins in WO02/12325 which function to enhance the apoptotic activity of p53. ASPP1 and ASPP2 selectively interact with p53 to enhance the apoptotic function of p53 at p53 responsive promoters to promote apoptosis *in vivo*. We herein describe the interaction of ASPP family members with 25 the oncogene Ras. ASPP 1 and 2 are also phophoproteins.

Ras oncogenes are frequently activated by mutation or over expression in many human tumours. For example, approximately 95% of pancreatic tumours contain so 30 called K-Ras mutations. Ras oncogenes are believed to exert their effect by overriding the normal cell-cycle control mechanisms by activating protein kinases (e.g. Raf, Mek, Erk kinase pathways) which regulate the function of cell-cycle cyclins which promote the proliferation of eukaryotic cells.

In its inactive state Ras is bound to GDP. The activation of Ras by growth factors results in exchange of GDP for GTP and a consequent change in the conformation of Ras to an activated form. In vitro, Ras has an intrinsic GTPase activity which 5 becomes active when growth factor stimulation is removed and returns Ras to its GDP bound state. Ras is also a post-translationally modified protein and it is this modification which facilitates the localisation of Ras to the cell membrane and allows Ras to receive growth factor signals. The post-translational modification is farnesylation which results in the alkylation of cysteine residues in a conserved motif 10 "CAAX". Ras has three CAAX motifs located in the C-terminus of the protein and it has been shown that inhibition of the farnesylation reaction of Ras blocks its processing and thereby inactivates the protein. The farnesylation reaction has been a target for the rational design of agents which inhibit the reaction thereby preventing the localisation of Ras at its site of action, the inner cell membrane. However, the 15 farnesylation reaction is more complicated than was first seemed. For example, H Ras is exclusively modified by farnesyltransferase whereas K-Ras and N-Ras can also be modified by geranylgeranyltransferase. This has meant that there is a continuing need to identify new targets which can modulate Ras activity or oncogenic Ras activity, either directly or indirectly,

20 We have identified ASPP 1/2 as Ras binding targets. The binding domain in ASPP1/2 is the amino terminus of the protein. We also show that Ras activates ASPP through the MAPK and Raf CX pathway and that dephosphorylation by phosphatase action is an important factor regulating ASPP action. The interaction of 25 these protein factors with ASPP provides an opportunity to identify agents which enhance or inhibit the action of ASPP on p53 mediated apoptosis.

According to an aspect of the invention there is provided method for the identification of agents which modulate the interaction of the proto-oncogene/oncogene Ras with the p53 binding protein family ASPP, either directly or 30 indirectly.

According to an aspect of the invention there is provided a screening method for the identification of agents which modulate the interaction of a first polypeptide encoded by a nucleic acid molecule selected from the group consisting of:

- 5 a) a polypeptide encoded by a nucleic acid molecule comprising a nucleic acid sequence as represented in Figure 17a or 17b;
- b) a polypeptide encoded by a nucleic acid molecule which hybridises to the nucleic acid molecule in (a) and which enhances the pro-apoptotic activity of p53;
- c) a polypeptide encoded by a nucleic acid molecule consisting of a nucleic acid sequence that is degenerate as a result of the genetic code to a nucleic acid molecule as defined in (a) and (b); with a second polypeptide selected from the group consisting of:
- 10 d) a polypeptide encoded by a nucleic acid molecule comprising a nucleic acid sequence as represented in Figure 18a, 18c, 18e or 18g;
- e) a polypeptide encoded by a nucleic acid molecule which hybridises to the nucleic acid molecule in (d) above and which has the activity associated with Ras, or a variant Ras polypeptide;
- f) a polypeptide encoded by a nucleic acid molecule consisting of a nucleic acid sequence that is degenerate as a result of the genetic code to a nucleic acid molecule as defined in (d) and (e); comprising,
- 20 i) forming a preparation comprising said first and second polypeptide;
- ii) adding at least one candidate agent to be tested; and
- iii) determining the effect, or not, of said agent on the interaction of said first polypeptide with said second polypeptide.

25

In a preferred method of the invention said first polypeptide is represented by the amino acid sequence as shown in Figure 17c or 17d, or a variant polypeptide wherein said variant polypeptide sequence has been altered by addition, substitution or deletion of at least one amino acid residue.

30

A variant polypeptide may differ in amino acid sequence by one or more substitutions, additions, deletions, truncations which may be present in any combination. Among preferred variants are those that vary from a reference polypeptide by conservative amino acid substitutions. Such substitutions are those that substitute a given amino acid by another amino acid of like characteristics. The following non-limiting list of amino acids are considered conservative replacements (similar): a) alanine, serine, and threonine; b) glutamic acid and asparatic acid; c) asparagine and glutamine d) arginine and lysine; e) isoleucine, leucine, methionine and valine and f) phenylalanine, tyrosine and tryptophan.

10

In addition, the invention features polypeptide sequences having at least 75% identity with the polypeptide sequence as hereindisclosed, or fragments and functionally equivalent polypeptides thereof. In one embodiment, the polypeptides have at least 85% identity, more preferably at least 90% identity, even more preferably at least 15 95% identity, still more preferably at least 97% identity, and most preferably at least 99% identity with the amino acid sequence illustrated herein.

In a further preferred method of the invention said first polypeptide comprises the amino acid sequence +1 to +120 of the sequence shown in Fig 17c and 17d 20 Preferably said polypeptide consists of the amino acid sequence +1 to +120 of the sequence shown in Figure 17c or 17d.

In a further preferred method of the invention said second polypeptide is represented by the amino acid sequence shown in Figure 18b, 18d, 18f or 18h, or a variant 25 polypeptide wherein said variant polypeptide sequence has been altered by addition, substitution or deletion of at least one amino acid residue.

In a preferred method of the invention said second polypeptide is modified at amino acid residue 12. Preferably said modification is the substitution of amino acid 12 for 30 amino acid valine. Preferably said second polypeptide is K-RasV12. Alternatively said polypeptide is H-RasV12.

In a yet further preferred method of the invention said second polypeptide is modified at amino acid residue 17. Preferably said modification is substitution of serine for asparagine at amino acid residue 17.

5

In a further preferred method of the invention said first and second polypeptides are expressed by a cell.

10 In a preferred method of the invention said cell is a cell transfected with at least one nucleic acid molecule(s) which encodes said first and second polypeptides.

Preferably the expression of said nucleic acid molecule(s) is regulatable.

In a preferred method of the invention said cell is a cancer cell.

15

In a yet further preferred method of the invention said cell is part of a transgenic animal wherein the genome of said animal has been modified to include nucleic acid molecules which encode first and second polypeptides. Preferably said nucleic acid molecules are expressed in a specific cell/tissue.

20

In a yet still further preferred method of the invention said preparation includes at least one chemotherapeutic agent.

25 According to an aspect of the invention there is provided a screening method for the identification of agents which modulate the phosphorylation of a first polypeptide encoded by a nucleic acid molecule selected from the group consisting of:

- a) a polypeptide encoded by a nucleic acid molecule comprising a nucleic acid sequence as represented in Figure 17a or 17b;
- b) a polypeptide encoded by a nucleic acid molecule which hybridises to the nucleic acid molecule in (a) and which enhances the pro-apoptotic activity of p53;

c) a polypeptide encoded by a nucleic acid molecule consisting of a nucleic acid sequence that is degenerate as a result of the genetic code to a nucleic acid molecule as defined in (a) and (b); with a second polypeptide selected from the group consisting of:

5 d) a polypeptide encoded by a nucleic acid molecule comprising a nucleic acid sequence as represented in Figure 19 or 20;

e) a polypeptide encoded by a nucleic acid molecule which hybridises to the nucleic acid molecule in (d) above and which has protein kinase activity;

f) a polypeptide encoded by a nucleic acid molecule consisting of a nucleic acid sequence that is degenerate as a result of the genetic code to a nucleic acid molecule as defined in (d) and (e); comprising,

10 i) forming a preparation comprising said first and second polypeptide;

ii) adding at least one candidate agent to be tested; and

iii) determining the effect, or not, of said agent on the phosphorylation state of

15 said first polypeptide.

According to a further aspect of the invention there is provided a screening method for the identification of agents which modulate the phosphorylation state of a first polypeptide encoded by a nucleic acid molecule selected from the group consisting of:

20 a) a polypeptide encoded by a nucleic acid molecule comprising a nucleic acid sequence as represented in Figure 17a or 17b;

b) a polypeptide encoded by a nucleic acid molecule which hybridises to the nucleic acid molecule in (a) and which enhances the pro-apoptotic activity of p53;

25 c) a polypeptide encoded by a nucleic acid molecule consisting of a nucleic acid sequence that is degenerate as a result of the genetic code to a nucleic acid molecule as defined in (a) and (b); with a second polypeptide selected from the group consisting of:

d) a polypeptide encoded by a nucleic acid molecule comprising a nucleic acid sequence as represented in Figure 21;

5 e) a polypeptide encoded by a nucleic acid molecule which hybridises to the nucleic acid molecule in (d) above and which has protein phosphatase activity;

f) a polypeptide encoded by a nucleic acid molecule consisting of a nucleic acid sequence that is degenerate as a result of the genetic code to a nucleic acid molecule as defined in (d) and (e); comprising,

i) forming a preparation comprising said first and second polypeptide;

ii) adding at least one candidate agent to be tested; and

iii) determining the effect, or not, of said agent on the phosphorylation state of said first polypeptide.

10

In a preferred method of the invention said agent is a polypeptide.

In a preferred method of the invention said polypeptide is an antibody, or active binding fragment thereof.

15

Preferably said antibody or binding fragment is a monoclonal antibody.

Antibodies or immunoglobulins (Ig) are a class of structurally related proteins consisting of two pairs of polypeptide chains, one pair of light (L) (low molecular weight) chain (κ or λ), and one pair of heavy (H) chains (γ , α , μ , δ and ϵ), all four linked together by disulphide bonds. Both H and L chains have regions that contribute to the binding of antigen and that are highly variable from one Ig molecule to another. In addition, H and L chains contain regions that are non-variable or constant. The L chains consist of two domains. The carboxy-terminal domain is essentially identical among L chains of a given type and is referred to as the "constant" (C) region. The amino terminal domain varies from L chain to L chain and contributes to the binding site of the antibody. Because of its variability, it is referred to as the "variable" (V) region. The variable region contains complementarity determining regions or CDR's which form an antigen binding pocket. The binding pockets comprise H and L variable regions which contribute to antigen recognition. It is possible to create single variable regions, so called single

chain antibody variable region fragments (scFv's). If a hybridoma exists for a specific monoclonal antibody it is well within the knowledge of the skilled person to isolate scFv's from mRNA extracted from said hybridoma via RT PCR. Alternatively, phage display screening can be undertaken to identify clones expressing scFv's.

5

Alternatively said fragments are "domain antibody fragments". Domain antibodies are the smallest binding part of an antibody (approximately 13kDa). Examples of this technology is disclosed in US6, 248, 516, US6, 291, 158, US6,127, 197 and EP0368684 which are all incorporated by reference in their entirety.

10

In a preferred method of the invention said antibody fragment is a single chain antibody variable region fragment.

In a further preferred embodiment of the invention said antibody is a humanised or

15 chimeric antibody.

A chimeric antibody is produced by recombinant methods to contain the variable region of an antibody with an invariant or constant region of a human antibody. A

humanised antibody is produced by recombinant methods to combine the

20 complementarity determining regions (CDRs) of an antibody with both the constant (C) regions and the framework regions from the variable (V) regions of a human antibody.

Chimeric antibodies are recombinant antibodies in which all of the V-regions of a

25 mouse or rat antibody are combined with human antibody C-regions. Humanised

antibodies are recombinant hybrid antibodies which fuse the complementarity determining regions from a rodent antibody V-region with the framework regions from the human antibody V-regions. The C-regions from the human antibody are also used. The complementarity determining regions (CDRs) are the regions within the N-

30 terminal domain of both the heavy and light chain of the antibody to where the majority of the variation of the V-region is restricted. These regions form loops at the

surface of the antibody molecule. These loops provide the binding surface between the antibody and antigen.

Antibodies from non-human animals provoke an immune response to the foreign 5 antibody and its removal from the circulation. Both chimeric and humanised antibodies have reduced antigenicity when injected to a human subject because there is a reduced amount of rodent (i.e. foreign) antibody within the recombinant hybrid antibody, while the human antibody regions do not elicit an immune response. This results in a weaker immune response and a decrease in the clearance of the antibody. 10 This is clearly desirable when using therapeutic antibodies in the treatment of human diseases. Humanised antibodies are designed to have less "foreign" antibody regions and are therefore thought to be less immunogenic than chimeric antibodies.

15 In a further preferred method of the invention said agent is a peptide, preferably a modified peptide.

It will be apparent to one skilled in the art that modification to the amino acid sequence of peptides which modulate the interaction of ASPP family members with polypeptides involved in regulating ASPP activity could enhance the binding and/or 20 stability of the peptide with respect to its target sequence. In addition, modification of the peptide may also increase the *in vivo* stability of the peptide thereby reducing the effective amount of peptide necessary to inhibit an interaction. This would advantageously reduce undesirable side effects which may result *in vivo*. Modifications include, by example and not by way of limitation, acetylation and 25 amidation.

In a preferred method of the invention said peptide is acetylated. Preferably said acetylation is to the amino terminus of said peptide.

30 In a further preferred method of the invention said peptide is amidated. Preferably said amidation is to the carboxyl-terminus of said peptide.

In a further preferred method of the invention said peptide is modified by both acetylation and amidation.

5 Alternatively, or preferably, said modification includes the use of modified amino acids in the production of recombinant or synthetic forms of peptides. It will be apparent to one skilled in the art that modified amino acids include, by way of example and not by way of limitation, 4-hydroxyproline, 5-hydroxylysine, N⁶-acetyllysine, N⁶-methyllysine, N⁶,N⁶-dimethyllysine, N⁶,N⁶,N⁶-trimethyllysine, 10 cyclohexy alanine, D-amino acids, ornithine. Other modifications include amino acids with a C₂, C₃ or C₄ alkyl R group optionally substituted by 1, 2 or 3 substituents selected from halo (e.g. F, Br, I), hydroxy or C₁-C₄ alkoxy.

Alternatively, peptides could be modified by, for example, cyclisation. Cyclisation is known in the art, (see Scott et al Chem Biol (2001), 8:801-815; Gellerman et al J. Peptide Res (2001), 57: 277-291; Dutta et al J. Peptide Res (2000), 8: 398-412; Ngoka and Gross J Amer Soc Mass Spec (1999), 10:360-363.

In a preferred method of the invention peptides according to the invention are 20 modified by cyclisation.

In a further preferred method of the invention said agent is an aptamer.

Nucleic acids have both linear sequence structure and a three dimensional structure 25 which in part is determined by the linear sequence and also the environment in which these molecules are located. Conventional therapeutic molecules are small molecules, for example, peptides, polypeptides, or antibodies, which bind target molecules to produce an agonistic or antagonistic effects. It has become apparent that nucleic acid molecules also have potential with respect to providing agents with 30 the requisite binding properties which may have therapeutic utility. These nucleic acid molecules are typically referred to as aptamers. Aptamers are small, usually

stabilised, nucleic acid molecules, which comprise a binding domain for a target molecule. A screening method to identify aptamers is described in US 5,270,163 which is incorporated by reference. Aptamers are typically oligonucleotides which may be single stranded oligodeoxynucleotides, oligoribonucleotides, or modified 5 oligodeoxynucleotide or oligoribonucleotides.

The term "modified" encompasses nucleotides with a covalently modified base and/or sugar. For example, modified nucleotides include nucleotides having sugars which are covalently attached to low molecular weight organic groups other than a 10 hydroxyl group at the 3' position and other than a phosphate group at the 5' position. Thus modified nucleotides may also include 2' substituted sugars such as 2'-O-methyl-; 2-O-alkyl; 2-O-allyl; 2'-S-alkyl; 2'-S-allyl; 2'-fluoro-; 2'-halo or 2-azido-ribose, carbocyclic sugar analogues a-anomeric sugars; epimeric sugars such as arabinose, xyloses or lyxoses, pyranose sugars, furanose sugars, and sedoheptulose.

15 Modified nucleotides are known in the art and include, by example and not by way of limitation, alkylated purines and/or pyrimidines; acylated purines and/or pyrimidines; or other heterocycles. These classes of pyrimidines and purines are known in the art and include, pseudoisocytosine; N4, N4-ethanocytosine; 8-hydroxy-
20 N6-methyladenine; 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil; 5-fluorouracil; 5-bromouracil; 5-carboxymethylaminomethyl-2-thiouracil; 5-carboxymethylaminomethyl uracil; dihydrouracil; inosine; N6-isopentyl-adenine; 1-methyladenine; 1-methylpseudouracil; 1-methylguanine; 2,2-dimethylguanine; 2-methyladenine; 2-methylguanine; 3-methylcytosine; 5-methylcytosine; N6-
25 methyladenine; 7-methylguanine; 5-methylaminomethyl uracil; 5-methoxy amino methyl-2-thiouracil; β -D-mannosylqueosine; 5-methoxycarbonylmethyluracil; 5-methoxyuracil; 2 methylthio-N6-isopentenyladenine; uracil-5-oxyacetic acid methyl ester; psueouracil; 2-thiacytosine; 5-methyl-2 thiouracil, 2-thiouracil; 4-thiouracil; 5-methyluracil; N-uracil-5-oxyacetic acid methylester; uracil 5—oxyacetic acid; 30 queosine; 2-thiacytosine; 5-propyluracil; 5-propylcytosine; 5-ethyluracil; 5-

ethylcytosine; 5-butyluracil; 5-pentyluracil; 5-pentylcytosine; and 2,6-diaminopurine; methylpsuedouracil; 1-methylguanine; 1-methylcytosine.

The aptamers of the invention are synthesised using conventional phosphodiester linked nucleotides and synthesised using standard solid or solution phase synthesis techniques which are known in the art. Linkages between nucleotides may use alternative linking molecules. For example, linking groups of the formula P(O)S, (thioate); P(S)S, (dithioate); P(O)NR'2; P(O)R'; P(O)OR6; CO; or CONR'2 wherein R is H (or a salt) or alkyl (1-12C) and R6 is alkyl (1-9C) is joined to adjacent nucleotides through -O- or -S-. The binding of aptamers to a target polypeptide is readily tested by assays hereindisclosed.

According to a further aspect of the invention there is provided a cell transfected with at least one nucleic acid molecule wherein the genome of said cell is modified to include at least one copy of a nucleic acid molecule encoding a polypeptide selected from the group consisting of:

- a) a polypeptide encoded by a nucleic acid molecule comprising a nucleic acid sequence as represented in Figure 17a or 17b;
- b) a polypeptide encoded by a nucleic acid molecule which hybridises to the nucleic acid molecule in (a) and which enhances the pro-apoptotic activity of p53;
- c) a polypeptide encoded by a nucleic acid molecule consisting of a nucleic acid sequence that is degenerate as a result of the genetic code to a nucleic acid molecule as defined in (a) and (b); and at least one copy of a nucleic acid molecule encoding a polypeptide selected from the group consisting of:
- d) a polypeptide encoded by a nucleic acid molecule comprising a nucleic acid sequence as represented in Figure 18a, 18c, 18e, or 18g;
- e) a polypeptide encoded by a nucleic acid molecule which hybridises to the nucleic acid molecule in (d) above and which has the activity associated with Ras or a variant Ras polypeptide;
- f) a polypeptide encoded by a nucleic acid molecule consisting of a nucleic acid

sequence that is degenerate as a result of the genetic code to a nucleic acid molecule as defined in (d) and (e) wherein said cell is adapted for the regulated expression of said nucleic acid molecules.

5 According to a further aspect of the invention there is provided a cell transfected with at least one nucleic acid molecule wherein the genome of said cell is modified to include at least one copy of a nucleic acid molecule encoding a polypeptide selected from the group consisting of:

- a) a polypeptide encoded by a nucleic acid molecule comprising a nucleic acid sequence as represented in Figure 17a or 17b;
- b) a polypeptide encoded by a nucleic acid molecule which hybridises to the nucleic acid molecule in (a) and which enhances the pro-apoptotic activity of p53;
- c) a polypeptide encoded by a nucleic acid molecule consisting of a nucleic acid sequence that is degenerate as a result of the genetic code to a nucleic acid molecule as defined in (a) and (b) and at least one copy of a nucleic acid molecule encoding a polypeptide selected from the group consisting of;
- d) a polypeptide encoded by a nucleic acid molecule comprising a nucleic acid sequence as represented in Figure 19a or 20a;
- e) a polypeptide encoded by a nucleic acid molecule which hybridises to the nucleic acid molecule in (d) above and which has protein kinase activity;
- f) a polypeptide encoded by a nucleic acid molecule consisting of a nucleic acid sequence that is degenerate as a result of the genetic code to a nucleic acid molecule as defined in (d) and (e) wherein said cell is adapted for the regulated expression of said nucleic acid molecules.

25 According to a yet further aspect of the invention there is provided a cell transfected with at least one nucleic acid molecule wherein the genome of said cell is modified to include at least one copy of a nucleic acid molecule encoding a polypeptide selected from the group consisting of:

- a) a polypeptide encoded by a nucleic acid molecule comprising a nucleic acid sequence as represented in Figure 17a or 17b;

b) a polypeptide encoded by a nucleic acid molecule which hybridises to the nucleic acid molecule in (a) and which enhances the pro-apoptotic activity of p53;

c) a polypeptide encoded by a nucleic acid molecule consisting of a nucleic acid sequence that is degenerate as a result of the genetic code to a nucleic acid molecule as defined in (a) and (b) and at least one copy of a nucleic acid molecule encoding a polypeptide selected from the group consisting of;

5 d) a polypeptide encoded by a nucleic acid molecule comprising a nucleic acid sequence as represented in Figure 21a;

e) a polypeptide encoded by a nucleic acid molecule which hybridises to the nucleic acid molecule in (d) above and which has protein kinase activity;

10 f) a polypeptide encoded by a nucleic acid molecule consisting of a nucleic acid sequence that is degenerate as a result of the genetic code to a nucleic acid molecule as defined in (d) and (e) wherein said cell is adapted for the regulated expression of said nucleic acid molecules.

15

In a preferred embodiment of the invention said cell further comprises a nucleic acid molecule which includes a reporter gene to monitor the activity of said pro-apoptotic polypeptide(s).

20 In a preferred embodiment of the invention said cell is a cancer cell.

According to a yet further aspect of the invention there is provided a non-human transgenic animal comprising at least one cell according to the invention.

25 In a preferred embodiment of the invention said non-human animal is a non-human primate.

In a further preferred embodiment of the invention said transgenic animal is a rodent, preferably a mouse, rat or hamster.

30

In an alternative preferred embodiment of the invention said transgenic animal is a pig.

It is well within the knowledge of the skilled person to successfully generate both a 5 heterozygous and homozygous transgenic animals with intergation of a desired nucleic acid encoding a particular gene or combination of genes using modified embryonic stem cells. These same steps can be easily applicable to species other than for example, mice. For example, Ware *et al* teaches an embryonic stem cell culture condition amenable for such animals as cattle, pigs and sheep (*Society for the* 10 *Study of Reproduction*, 38:241 (1988)). In addition, this reference illustrates that the state of the art with respect to generation of transgenic species, other than mice, using modified embryonic stem cells is a well developed methodology.

An embodiment of the invention will now be described by example only and with 15 reference to the following Figures:

Figure 1 illustrates the domains within ASPP2 which mediate ASPP2 activity;

Figure 2 illustrates that both H-ras V12 and K-ras V12 activate the ASPP2 and p53 20 synergy. Plasmids expressing CMV, p53, ASPP2 and ASPP2 + p53 were transfected in Saos-2 cells either with 1.5 μ g of an empty vector, oncogenic H-ras or oncogenic K-ras. All samples were co-transfected with a bax-luciferase reporter. A. A transactivation assay was performed and shown here is the fold activation over p53. The average of duplicate samples are shown. B, C and D. Western blot of the samples 25 used for transactivation. B. Expression of H-ras V12 and K-ras V12. C. Expression of ASPP2 and p53 for samples co-transfected with H-rasV12. D. Expression of ASPP2 and p53 for samples co-transfected with K-rasV12;

Figure 3 illustrates that average H-ras V12 and K-ras V12 activation of ASPP2 and 30 p53 synergy;

Figure 4 illustrates Ras and Ras V12 activation of ASPP2 & p53 synergy on different promoters. Plasmids expressing CMV, p53, ASPP2 and ASPP2 + p53 were transfected either with 1 μ g of an empty vector, wild type H-ras, dominant negative H-ras N17 or oncogenic H-ras V12. All these samples were co-transfected with the indicated reporter. Luciferase activity was determined and the values are in relative luminescent units. The fold activation over p53 is shown. **A.** Bax-luciferase reporter, **B.** PIG3-luciferase reporter, **C.** Mdm2-luciferase reporter. **D.** The effect of H-rasV12 on ASPP2 and p53 activity on different reporters is shown. **E.** The fold activation of K-ras V12 and H-rasV12 over p53 and ASPP2 with the Bax-luciferase and the Mdm2-luciferase reporters.;

Figure 5 illustrates that oncogenic Ras activates endogenous ASPP1/2 and p53 to transactivate Bax-luciferase reporter. **A.** U2OS cells were transfected with 1 μ g of either control vector or H-ras V12, each of which was also transfected with 6 μ g of plasmids expressing either PCDNA or anti-sense ASPP2. All samples were co-transfected with bax-luciferase reporter. The lysates were then tested for luciferase levels. The values shown above are averages of duplicates. **B.** U2OS cells were transfected with 1 μ g of a control vector pEF, H-ras V12 or K-ras V12, each of which were then co-transfected with 6 μ g of plasmids expressing either PCDNA, anti-sense (α) ASPP1, α ASPP2, or E6, or 4 μ g of iASPP. All samples were co-transfected with Bax-luciferase. A transactivation assay was done on the lysates. The fold activation above the value of pEF and PCDNA control is shown. All samples were done in duplicate and the mean is shown here;

Figure 6A illustrates the testing of H-ras and K-ras RNAi constructs in pSUPPRESSOR and pSUPER vectors. Both HA-tagged H-rasV12 and HA-tagged K-rasV12 were co-transfected with either H-ras pSUPPRESSOR, K-ras pSUPPRESSOR, H-ras pSUPER or K-ras pSUPER. A western blot was performed with an HA antibody to see whether the different RNAi constructs were able inhibit expression in a specific manner. Effect of Ras RNAi on ASPP2 transactivation activity. Figure 6B illustrates H-ras pSUPER and K-ras pSUPER co-transfected with

ASPP2 and/or p53 and its effect as monitored by the PIG3-luciferase counts. Figure 6C. A western blot was performed for each sample and blotted for ASPP2 and p53;

Figure 7 illustrates that activated Raf increases ASPP2 activity. **A.** p53 and ASPP2 were co-transfected with wild-type H-ras, dominant negative Ras N17, oncogenic H-ras V12 or Raf CX together with Bax-luciferase reporter. The values shown are the fold increase over p53 alone; Figure 7B and 7C illustrate activated Raf increases ASPP2 activity. **B.** p53 and ASPP2 were transfected with or without Raf CX. All samples were co-transfected with bax-luciferase. **C.** A western blot was performed with the samples shown in 7B and blotted against ASPP2, Raf and p53. Figure 7D illustrates that activated Raf increases ASPP2 activity. Raf CX increases p53 and ASPP2 synergy 2.5 fold (average of 3 experiments);

Figure 8 illustrates *in vitro* phosphorylation of the C-terminus of ASPP2. **A.** Small scale screening of ASPP2 phosphorylation by MAPK1, p70S6K, p90rsk, PKA, PKB and p83SAPK. The appropriate enzyme was added to a reaction containing P32 and either H2B as a positive control, ASPP2 or no substrate. **B.** A large scale *in vitro* phosphorylation assay was performed with ATP at higher P32 counts. PKA, p38SAPK, MAPK1 and p90rsk were used as kinases. The cpm counts of each band was measured and shown in **C.** **D.** The ASPP2 protein phosphorylated by MAPK was trypsinized and put through a High Performance Liquid Chromatography. The radioactive peptide fragments were collected and analysed by mass spectrometry. The second radioactive peak corresponds to a region of ASPP2 containing a putative MAPK phosphorylation site;

Figure 9 illustrates ASPP2 phosphorylation mutants. Three ASPP2 point mutants were made by replacing serines by alanine. Mutant 1 has a putative MAPK site mutated (PRPLSPT). Mutant 2 has the two serines at the putative PKA site mutated (TASSESP) and mutant 3 has the *in vitro* phosphorylated MAPK site mutated (PAPSPG);

Figure 10 illustrates that RafCX is not able to transactivate ASPP2 mutant3. A. ASPP2 wild type and mutants were transfected in Saos2 cells with or without p53 and Bax-luciferase reporter activity measured. B. Bax-luciferase, ASPP2 wild type and mutants were transfected with p53 and with or without 1.5 ug of RafCX. The values shown are the fold over ASPP2 and p53. This is the average of 3 experiments;

Figure 11 illustrates that endogenous ras binds the N-terminus of ASPP1. A. ASPP1 fragments that either contain or lack the ras-association domain (RAD). The column on the right shows the prediction for the different fragments to bind ras. B. U2OS cells were transfected with 10 ug of the different ASPP1 fragments. Lysates were made and endogenous ras immunoprecipitated with the 238 antibody. The immunoprecipitations were run on a gel and western blotted, probed with V5 to visualize the ASPP1 fragments. The left panel is the input and the right panel the immunoprecipitation;

Figure 12 illustrates that endogenous ras binds ASPP2 after EGF stimulation: An inducible ASPP2 clone was used for an immunoprecipitation of endogenous ras. The cells were starved overnight, and then either stimulated with EGF or induced for ASPP2 expression or both simultaneously. The left panel shows ASPP2 and ras input whereas the right panel shows the immunoprecipitation of ras (238 antibody) and the immunoprecipitation with the control antibody (IgG);

Figure 13: illustrates that endogenous ASPP1 and ASPP2 bind endogenous activated ras. Saos2 cells were used for an immunoprecipitation of ASPP1 and ASPP2. The cells were starved overnight or grown in EGF and 20% fetal calf serum overnight. The western blot shows that Ras binds ASPP2 slightly more efficiently after EGF and 20%FCS stimulation. Endogenous ras is only co-immunoprecipitated by ASPP1 after the cells have been stimulated with EGF and FCS;

Figure 14 illustrates that purified N-term ASPP1 binds directly in a preferential manner to Ras.GTP. A. Purified ras was loaded with tritium labelled-GDP, -GTP or

not loaded as a control. The cpm counts of the tritium are shown. The differences in cpm is due to the fact that GDP and GTP were not tritium-labelled at the same level. **B.** Relative loading of ras-GDP and ras-GTP, showing the mol of nucleotide bound to ras. Both ras-GDP and ras-GTP were loaded with an equal amount of nucleotide. **C.** Loaded ras-GDP and ras-GTP with or without purified N-terminus ASPP1 was immunoprecipitated with a V5 antibody against the ASPP1 fragment. The immunoprecipitations were western blotted against ras to see whether there was direct and preferential binding of ras-GDP and ras-GTP to the amino-terminus of ASPP1. **D.** The intensity of the ras-GDP and ras-GTP bands pulled down by N-term ASPP1 were measured and shown as a graph. N-terminus ASPP1 binds ras-GTP four fold more strongly than it does to ras-GDP;

Figure 15 illustrates that ASPP2 co-localizes with H-ras V12. U2OS cells co-transfected with ASPP2 and H-rasV12 show co-localization of both proteins at the plasma membrane of the cells;

Figure 16 illustrates that K-rasV12 affects ASPP1 localization in a MAPK-dependent manner. After co-transfection of K-rasV12, ASPP1 changes its sub-cellular localization forming dense doughnut-like shapes. This change in localization is dependent on MAPK as a MAPK inhibitor UO126 reverts this change in localization;

Figure 17a is the ASPP1 nucleic acid sequence; Figure 17b is the ASPP2 nucleic acid sequence; Figure 17c is the ASPP1 protein sequence; Figure 17d is the ASPP2 protein sequence;

Figure 18a is the H-Ras wild-type nucleic acid sequence; Figure 18b is the H-Ras protein sequence; Figure 18c is the H-Ras oncogenic nucleic acid sequence; Figure 18d is the H-Ras oncogenic protein sequence; Figure 18e is the K Ras wild-type nucleic acid sequence; Figure 18f is the wild-type K-Ras protein sequence; Figure

18g is the K-Ras oncogenic nucleic acid sequence; and Figure 18h is the K-Ras oncogenic protein sequence;

5 Figure 19a is the MAPK nucleic acid sequence; Figure 19b is the MAPK protein sequence;

Figure 20a is the PKA nucleic acid sequence; Figure 20b is the PKA protein sequence;

10 Figure 21a is the phosphatase 1 nucleic acid sequence; Figure 21b is the phosphatase 1 protein sequence; and

Figure 22 illustrates the effect of H-ras RNAi and K-ras RNAi on apoptosis.

15 **EXAMPLE 1**

The amino terminus of ASPP1 and ASPP2 is necessary for its full activity

p53 is the most common tumour suppressor protein found mutated in cancers with more than half of all human cancers carrying p53 mutations. p53 is activated by 20 stress signals such as DNA damage and its activation can lead to one of two responses: cell cycle arrest or apoptosis. It has recently been shown that a novel family of tumour suppressor proteins, known as the ASPP family, can interact with p53 and specifically enhance p53-induced apoptosis but not cell-cycle arrest. ASPP1 and ASPP2 enhance the DNA binding and transactivation function of p53 on the 25 promoters of pro-apoptotic genes only in vivo. Mutant ASPP1 and ASPP2 missing the first 150 amino acids are not fully functional, suggesting that the domain is essential for full activity of the ASPP proteins. This amino-terminal domain that is required for ASPP activity contains a putative Ras-association domain (see Figure 1).

30 **EXAMPLE 2**

Oncogenic H-rasV12 and K-rasV12 increases ASPP2 transactivation activity

It has previously been reported that ASPP2 can increase p53 transactivation on pro-apoptotic genes and we wanted to see whether ras would have any effect on ASPP2 activity. We have shown, using transactivation assays, that both oncogenic H-rasV12 and K-rasV12 can increase ASPP2 activity 2-3 fold (see figure 2 and 3) on pro-apoptotic p53 reporters. Knowing that oncogenic RasV12 could activate ASPP2 activity, the roles of wild type Ras and its dominant negative version (Ras N17) were investigated. Interestingly, wild type H-ras seemed to have no effect on ASPP2 and p53 synergy whereas dominant negative ras reduced significantly the synergy, suggesting that endogenous ras activiy is needed for the full activity of ASPP2 on the bax-luciferase reporter (Figure 4A). To see whether the induction of ASPP activity by Ras is promoter specific, different p53 reporters were compared: both pro-apoptotic (such as Bax-luciferase and PIG3-luciferase) and non-apoptotic (Mdm2-luciferase). We can see that in all cases oncogenic ras activates ASPP2 2-3 fold irrespective of the promoter (figure 4A-C). Although there does not seem to be any promoter specificity regarding ras activation of ASPP (figure 4E), since ASPP2 has an intrinsic pro-apoptotic activity and only activates p53 transactivation on pro-apoptotic reporters, the overall effect of Ras is to significantly increase ASPP2 activity on pro-apoptotic reporters. (Figure 4D).

EXAMPLE 3

Oncogenic ras can activate endogenous ASPP1, ASPP2 and p53 to transactivate a pro-apoptotic reporter

U2OS cells were used to look at the effect of oncogenic ras on endogenous ASPP2 and p53. Figure 5A shows that H-ras V12 increases the bax-luciferase counts and that this inhibition is inhibited in the presence of anti-sense ASPP2, suggesting that the activity is via endogenous ASPP2. Both ASPP1 and ASPP2 seem necessary for the pro-apoptotic activity of H-rasV12 and K-rasV12. Removal of endogenous ASPP1/2

by anti-sense DNA inhibits oncogenic ras activation to the same levels as adding iASPP (figure 5B). The addition of the p53-inhibitor E6 also reduces oncogenic ras activation of bax-luciferase significantly. These results suggest that oncogenic ras can activate bax-luciferase via endogenous ASPP1, ASPP2 and p53.

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EXAMPLE 4

Endogenous H-ras is necessary for full ASPP2 activity

10 H-ras and K-ras RNAi constructs were made in both the pSUPPRESSOR and pSUPER vectors. Only the constructs in the pSUPER vector were able to reduce ras levels specifically as shown in Figure 6A. The pSUPER constructs were therefore tested in a transactivation assay and H-ras RNAi was able to reduce ASPP2 and p53 transcriptional activity as shown in Figure 6B. All the constructs were expressed 15 (Figure 6C) although there was no difference in ras levels after H-ras RNAi or K-ras RNAi (figure not shown); this is probably due to the very high endogenous levels of ras in those cells.

EXAMPLE 5

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Ras activates ASPP2 via its Raf-MAPK pathway

Ras is a GTPase which is upstream of many effector pathways, the most well-known of which is the Raf-MAPK pathway. As it was unclear as to whether ras activated 25 ASPP2 directly or via one of its pathways, we looked to see whether an activated form of Raf had any effect on ASPP2 activity. Figure 7 shows that Raf CAAX (an activated form of Raf) could increase ASPP2 and p53 synergy at least as much as H-rasV12, suggesting that oncogenic ras activates ASPP2 via its Raf pathway.

30 **EXAMPLE 6**

The C-term of ASPP2 is phosphorylated in vitro by MAPK and Raf CX is unable to activate a phosphorylation mutant of ASPP2

The purified C-terminus of ASPP2 was used as a substrate to screen for kinases in an in vitro assay. An array of kinases were added to the purified C-terminus of ASPP2 and the phosphorylation status of the protein was analysed using P32 as a phosphorylation marker. MAPK1, PKA, p38SAPK and p90rsk were all found to be able to phosphorylate ASPP2 (figure 8A). A larger scale in vitro phosphorylation assay was then performed, using the four enzymes that had screened positive in the first round (figure 8B-C). The phosphorylated fragment of ASPP2 was run on a gel, exposed, extracted from the gel and trypsinized. The trypsinized protein was then put through a High Performance Liquid Chromatography (HPLC) with an acetonitrile gradient, the radioactive peptides were then collected and analyzed by mass spectrometry (figure 8D). For the MAPK-phosphorylated ASPP2 C-terminus, there were two phosphorylation sites. The first one corresponded to the linker region between the GST and the protein. The second phosphorylated site corresponded to a region of the protein that contains a MAPK-consensus sequence phosphorylation site; PAPSPGL.

ASPP2 phosphorylation mutants were then constructed to see whether this site is phosphorylated in vivo. A serine was replaced by an alanine residue at the MAPK phosphorylation site identified by the in vitro phosphorylation assay (mutant 3), at another MAPK putative site (mutant 1) and at a PKA putative site that was shown to be phosphorylated in vitro (mutant 2) as shown in figure 9.

The ASPP2 mutants were compared to wild type ASPP2 in a transactivation assay with p53 using bax-luciferase as a reporter (figure 10A). The activity of all three ASPP2 mutants were equivalent to ASPP2 wild type activity. We then wanted to see if RafCX was able to increase ASPP2 wild type and mutants activity. p53 and ASPP2 wild type or mutants were transfected with and without RafCX and the bax-luciferase reporter activity measured. The values shown in Figure 10B show the fold of

activation of RafCX over p53 and ASPP2 values. RafCX is shown to increase ASPP2 wild type, mutant 1 and mutant 2 activity but not ASPP2 mutant 3 activity. ASPP2 mutant three is mutated in the putative MAPK site that was shown to phosphorylate ASPP2 in vitro. This suggests that RafCX, by activating its downstream effector pathway MAPKK-MAPK, leads to MAPK phosphorylation of ASPP2 at the serine site PAPSPGL (amino acid 827) and that phosphorylation on this serine is necessary for RafCX activation of ASPP2.

EXAMPLE 8

10 H-ras binds to ASPP1 in its amino-terminus

As ASPP1 and ASPP2 contain a putative ras-association domain in their amino-terminus, we investigated whether ASPP was able to bind ras. We used different 15 fragments of ASPP1 to see what parts of the protein bound to ras (figure 11A). Fragment 1 contains the N-terminus of the protein, fragment 2 lacks the C-terminus, KIA lacks part of the ras-association domain, fragment 6 lacks the entire ras-association domain and fragment 8 contains only the carboxy-terminus. Endogenous ras was immunoprecipitated and the fragments blotted for by western blot. As figure 20. 11B shows, all fragments containing the putative ras-association domain (full length ASPP1, fragment 1 and fragment 2) were pulled down by endogenous ras. The fragments lacking the ras-association domain (fragment 6 and fragment 8) were unable to bind to endogenous ras. Fragment KIA which contained part of the ras association domain was immunoprecipitated by endogenous ras; this might be due to 25 this fragment heterodimerizing with full-length, wild-type endogenous ASPP1 which contains the entire ras-association domain.

EXAMPLE 9

30 Activated endogenous ras binds ASPP1 and ASPP2

EGF ligand activates EGFR, which leads to the recruitment of a guanine nucleotide exchange factor (GNEF). Once recruited to the plasma membrane and in close proximity to Ras, the GNEF leads to the exchange of GDP- to GTP-associated ras, making ras active and able to activate its downstream effectors. Thus EGF is able to

5 activate endogenous ras in a physiological manner. An ASPP2 inducible clone was used to see whether endogenous, wild-type ras bound ASPP2 with different activity after stimulation with EGF. An immunoprecipitation was performed with endogenous ras, with and without ASPP2 and ras induction. Figure 12 shows that there is very little background binding of endogenous ras and endogenous ASPP2

10 after cells have been starved for 24 hours. Inducing ASPP2 expression shows a small band of ASPP2 being co-immunoprecipitated by endogenous ras. Inducing endogenous ras by EGF and foetal calf serum leads to a significant increase in ras and ASPP2 binding.

15 An immunoprecipitation was performed to determine whether endogenous ras is able to bind to endogenous ASPP1 and ASPP2. Figure 13 shows that induced ras is co-immunoprecipitated with endogenous ASPP1, whereas non-induced ras was not able to bind to ASPP1. Although the difference in binding of ASPP2 to induced versus non-induced ras was not as clear, we can still see a slight increase of ASPP2 binding

20 to induced ras compared to non-induced ras.

EXAMPLE 10

The amino-terminus of ASPP1 binds ras.GTP more efficiently than ras.GDP

25 In order to determine whether the interaction of ras and ASPP1/2 is direct, as we would expect if ASPP contains an active ras-association domain, we performed an in vitro binding assay with purified ras and amino-terminus of ASPP1. As suggested with the EGF-dependent binding of ras to ASPP, we speculated that ras in its GTP form could bind the amino-terminus of ASPP1 more efficiently than ras in its GDP form. We therefore purified ras and loaded it with either GDP or GTP (figure 14A-

B). The loaded ras was mixed with the purified amino-terminus-ASPP1 or without it as a control and the amino-terminus of ASPP1 was immunoprecipitated with a V5 antibody. As figure 14C-D shows, the N-terminus of ASPP1 binds ras-GTP with four-fold more efficiency than to ras-GDP.

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EXAMPLE 11

Oncogenic ras co-localizes with ASPP2 but not ASPP1 and changes the ASPP1 cellular localization.

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U2OS cells co-transfected with oncogenic H-rasV12 and ASPP2 clearly show co-localization at the plasma membrane of the cells (figure 15). However H-rasV12 and ASPP1 are not seen to co-localize. ASPP1, unlike ASPP2, is not found at the plasma membrane (figure 16). After co-transfection of K-rasV12, ASPP1 forms dense 15 doughnut-like shapes in the middle of the cells. However, after addition of a MAPK-inhibitor UO126, ASPP1 resumes its “normal” cellular localization pattern.

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Claims

1. A screening method for the identification of agents which modulate, either directly or indirectly, the interaction of a first polypeptide encoded by a nucleic acid molecule selected from the group consisting of:
 - 5 a) a polypeptide encoded by a nucleic acid molecule comprising a nucleic acid sequence as represented in Figure 17a or 17b;
 - b) a polypeptide encoded by a nucleic acid molecule which hybridises to the nucleic acid molecule in (a) and which enhances the pro-apoptotic activity of p53;
 - 10 c) a polypeptide encoded by a nucleic acid molecule consisting of a nucleic acid sequence that is degenerate as a result of the genetic code to a nucleic acid molecule as defined in (a) and (b); with a second polypeptide selected from the group consisting of:
 - d) a polypeptide encoded by a nucleic acid molecule comprising a nucleic acid sequence as represented in Figure 18a, 18c, 18e or 18g;
 - 15 e) a polypeptide encoded by a nucleic acid molecule which hybridises to the nucleic acid molecule in (d) above and which has the activity associated with Ras or a variant Ras polypeptide;
 - f) a polypeptide encoded by a nucleic acid molecule consisting of a nucleic acid sequence that is degenerate as a result of the genetic code to a nucleic acid molecule as defined in (d) and (e); comprising,
 - i) forming a preparation comprising said first and second polypeptide;
 - ii) adding at least one candidate agent to be tested; and
 - iii) determining the effect, or not, of said agent on the interaction of said first polypeptide with said second polypeptide.
- 20 2. A method according to Claim 1 wherein said first polypeptide is represented by the amino acid sequence as shown in Figure 17c or 17d, or a variant polypeptide wherein said variant polypeptide sequence has been altered by addition, substitution or deletion of at least one amino acid residue.
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3. A method according to Claim 1 or 2 wherein said first polypeptide comprises the amino acid sequence +1 to +120 of the sequence shown in Fig 17c and 17d.

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4. A method according to Claim 3 wherein said polypeptide consists of the amino acid sequence +1 to +120 of the sequence shown in Figure 17c or 17d.

10 5. A method according to any of Claims 1-4 wherein said second polypeptide is represented by the amino acid sequence shown in Figure 18b, 18d, 18f or 18h, or a variant polypeptide wherein said variant polypeptide sequence has been altered by addition, substitution or deletion of at least one amino acid residue.

15 6 A method according to Claim 5 wherein said second polypeptide comprises the amino acid sequence as shown in Figure 18d.

7. A method according to Claim 5 or 6 wherein said second polypeptide comprises the amino acid sequence as shown in Figure 18h.

20 8. A method according to any of Claims 1-4 wherein said second polypeptide is modified at amino acid residue 17.

9. A method according to Claim 8 wherein said modification is the substitution of a serine amino acid for an asparagine amino acid.

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10. A method according to any of Claims 1-9 wherein said first and second polypeptides are expressed by a cell.

30 11. A method according to Claim 10 wherein said cell is a cell transfected with at least one nucleic acid molecule(s) which encodes said first and second polypeptides.

12. A method according to Claim 10 or 11 wherein the expression of said nucleic acid molecule(s) is regulatable.

13. A method according to any of Claims 10-12 wherein said cell is a cancer cell.

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14. A method according to any of Claims 10-13 wherein said cell is part of a transgenic animal wherein the genome of said animal has been modified to include nucleic acid molecules which encode first and second polypeptides.

10 15. A method according to any of Claims 10-14 wherein said nucleic acid molecules are expressed in a specific cell/tissue.

15 16. A screening method for the identification of agents which modulate, either directly or indirectly, the phosphorylation of a first polypeptide encoded by a nucleic acid molecule selected from the group consisting of:

a) a polypeptide encoded by a nucleic acid molecule comprising a nucleic acid sequence as represented in Figure 17a or 17b;

b) a polypeptide encoded by a nucleic acid molecule which hybridises to the nucleic acid molecule in (a) and which enhances the pro-apoptotic activity of p53;

20 c) a polypeptide encoded by a nucleic acid molecule consisting of a nucleic acid sequence that is degenerate as a result of the genetic code to a nucleic acid molecule as defined in (a) and (b); with a second polypeptide selected from the group consisting of:

d) a polypeptide encoded by a nucleic acid molecule comprising a nucleic acid sequence as represented in Figure 19a or 20a;

e) a polypeptide encoded by a nucleic acid molecule which hybridises to the nucleic acid molecule in (d) above and which has protein kinase activity;

f) a polypeptide encoded by a nucleic acid molecule consisting of a nucleic acid sequence that is degenerate as a result of the genetic code to a nucleic acid molecule as defined in (d) and (e); comprising,

30 i) forming a preparation comprising said first and second polypeptide;

- ii) adding at least one candidate agent to be tested; and
- iii) determining the effect, or not, of said agent on the phosphorylation state of said first polypeptide.

5. 17. A screening method for the identification of agents which modulate, either directly or indirectly, the phosphorylation state of a first polypeptide encoded by a nucleic acid molecule selected from the group consisting of:

- a) a polypeptide encoded by a nucleic acid molecule comprising a nucleic acid sequence as represented in Figure 17a or 17b;
- 10 b) a polypeptide encoded by a nucleic acid molecule which hybridises to the nucleic acid molecule in (a) and which enhances the pro-apoptotic activity of p53;
- c) a polypeptide encoded by a nucleic acid molecule consisting of a nucleic acid sequence that is degenerate as a result of the genetic code to a nucleic acid molecule as defined in (a) and (b); with a second polypeptide selected from the group 15 consisting of:
- d) a polypeptide encoded by a nucleic acid molecule comprising a nucleic acid sequence as represented in Figure 21a;
- e) a polypeptide encoded by a nucleic acid molecule which hybridises to the nucleic acid molecule in (d) above and which has protein phosphatase activity;
- 20 f) a polypeptide encoded by a nucleic acid molecule consisting of a nucleic acid sequence that is degenerate as a result of the genetic code to a nucleic acid molecule as defined in (d) and (e); comprising,
- i) forming a preparation comprising said first and second polypeptide;
- ii) adding at least one candidate agent to be tested; and
- 25 iii) determining the effect, or not, of said agent on the phosphorylation state of said first polypeptide.

18. A method according to any of Claims 1-17 wherein said agent is a polypeptide.

19. A method according to Claim 18 wherein said polypeptide is an antibody, or active binding fragment thereof.

20. A method according to Claim 19 wherein said antibody or binding fragment
5 is a monoclonal antibody.

21. A method according to Claim 19 or 20 wherein said antibody fragment is a single chain antibody variable region fragment or a domain antibody fragment.

10 22. A method according to Claim 19 or 20 wherein said antibody is a humanised or chimeric antibody.

23. A method according to any of Claims 1-17 wherein said agent is a peptide.

15 24. A method according to any of Claims 1-17 wherein said agent is an aptamer.

25. A cell transfected with at least one nucleic acid molecule wherein the genome of said cell is modified to include at least one copy of a nucleic acid molecule encoding a polypeptide selected from the group consisting of:
20 a) a polypeptide encoded by a nucleic acid molecule comprising a nucleic acid sequence as represented in Figure 17a or 17b;
b) a polypeptide encoded by a nucleic acid molecule which hybridises to the nucleic acid molecule in (a) and which enhances the pro-apoptotic activity of p53;
c) a polypeptide encoded by a nucleic acid molecule consisting of a nucleic acid sequence that is degenerate as a result of the genetic code to a nucleic acid molecule as defined in (a) and (b); and at least one copy of a nucleic acid molecule encoding a polypeptide selected from the group consisting of:
25 d) a polypeptide encoded by a nucleic acid molecule comprising a nucleic acid sequence as represented in Figure 18a, 18c, 18e or 18g;
e) a polypeptide encoded by a nucleic acid molecule which hybridises to the
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nucleic acid molecule in (d) above and which has the activity associated with Ras or a variant Ras polypeptide;

5 f) a polypeptide encoded by a nucleic acid molecule consisting of a nucleic acid sequence that is degenerate as a result of the genetic code to a nucleic acid molecule as defined in (d) and (e) wherein said cell is adapted for the regulated expression of said nucleic acid molecule(s).

26. A cell transfected with at least one nucleic acid molecule wherein the genome of said cell is modified to include at least one copy of a nucleic acid molecule 10 encoding a polypeptide selected from the group consisting of:

10 a) a polypeptide encoded by a nucleic acid molecule comprising a nucleic acid sequence as represented in Figure 17a or 17b;
b) a polypeptide encoded by a nucleic acid molecule which hybridises to the nucleic acid molecule in (a) and which enhances the pro-apoptotic activity of p53;
15 c) a polypeptide encoded by a nucleic acid molecule consisting of a nucleic acid sequence that is degenerate as a result of the genetic code to a nucleic acid molecule as defined in (a) and (b) and at least one copy of a nucleic acid molecule encoding a polypeptide selected from the group consisting of;
d) a polypeptide encoded by a nucleic acid molecule comprising a nucleic acid 20 sequence as represented in Figure 19a or 20a;
e) a polypeptide encoded by a nucleic acid molecule which hybridises to the nucleic acid molecule in (d) above and which has protein kinase activity;
f) a polypeptide encoded by a nucleic acid molecule consisting of a nucleic acid sequence that is degenerate as a result of the genetic code to a nucleic acid 25 molecule as defined in (d) and (e) wherein said cell is adapted for the regulated expression of said nucleic acid molecule(s).

27. A cell transfected with at least one nucleic acid molecule wherein the genome of said cell is modified to include at least one copy of a nucleic acid molecule 30 encoding a polypeptide selected from the group consisting of:

a) a polypeptide encoded by a nucleic acid molecule comprising a nucleic acid

sequence as represented in Figure 17a or 17b;

b) a polypeptide encoded by a nucleic acid molecule which hybridises to the nucleic acid molecule in (a) and which enhances the pro-apoptotic activity of p53;

c) a polypeptide encoded by a nucleic acid molecule consisting of a nucleic acid sequence that is degenerate as a result of the genetic code to a nucleic acid molecule as defined in (a) and (b) and at least one copy of a nucleic acid molecule encoding a polypeptide selected from the group consisting of;

5 d) a polypeptide encoded by a nucleic acid molecule comprising a nucleic acid sequence as represented in Figure 21a;

10 b) a polypeptide encoded by a nucleic acid molecule which hybridises to the nucleic acid molecule in (d) above and which has protein phosphatase activity;

c) a polypeptide encoded by a nucleic acid molecule consisting of a nucleic acid sequence that is degenerate as a result of the genetic code to a nucleic acid molecule as defined in (d) and (e) wherein said cell is adapted for the regulated 15 expression of said nucleic acid molecule(s).

28. A cell according to any of Claims 25-27 wherein said cell further comprises a nucleic acid molecule which includes a reporter gene to monitor the activity of said pro-apoptotic polypeptide(s).

20 29. A cell according to any of Claims 25-28 wherein said cell is a cancer cell.

30. A non-human transgenic animal comprising at least one cell according to any of Claims 25-29.

25 31. An animal according to Claim 30 wherein said non-human animal is a non-human primate.

32. An animal according to Claim 30 wherein said transgenic animal is a rodent.

30 33. An animal according to Claim 30 wherein said transgenic animal is a pig.

Abstract

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Screening Assay

The invention relates to an screening assay for the identification of agents which modulate the activity of polypeptides which affect the apoptotic activity of the tumour suppressor protein p53.

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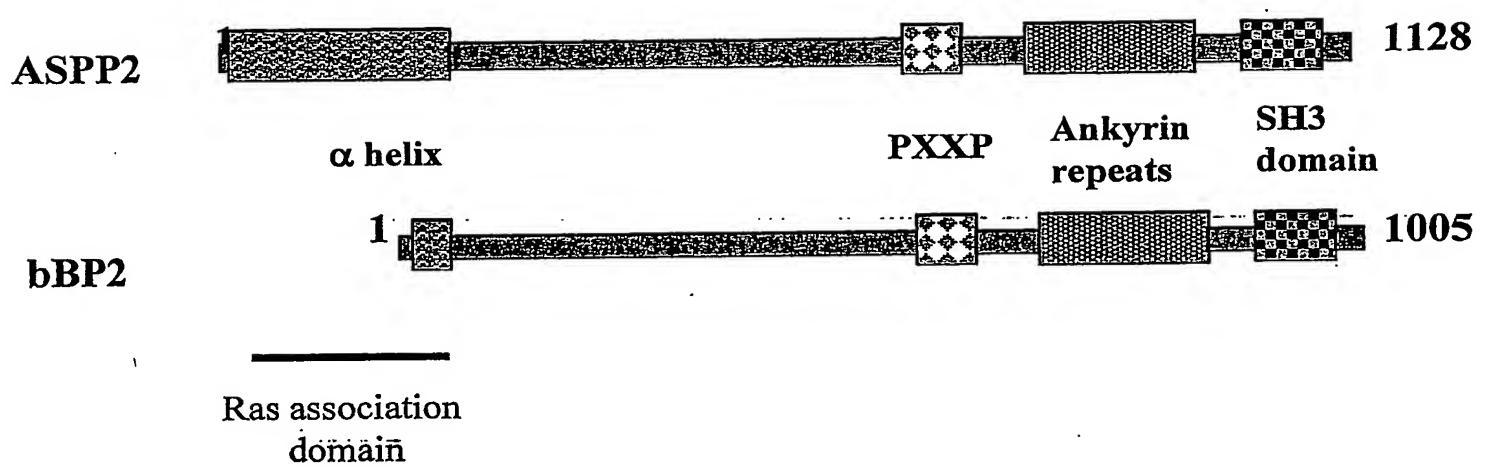
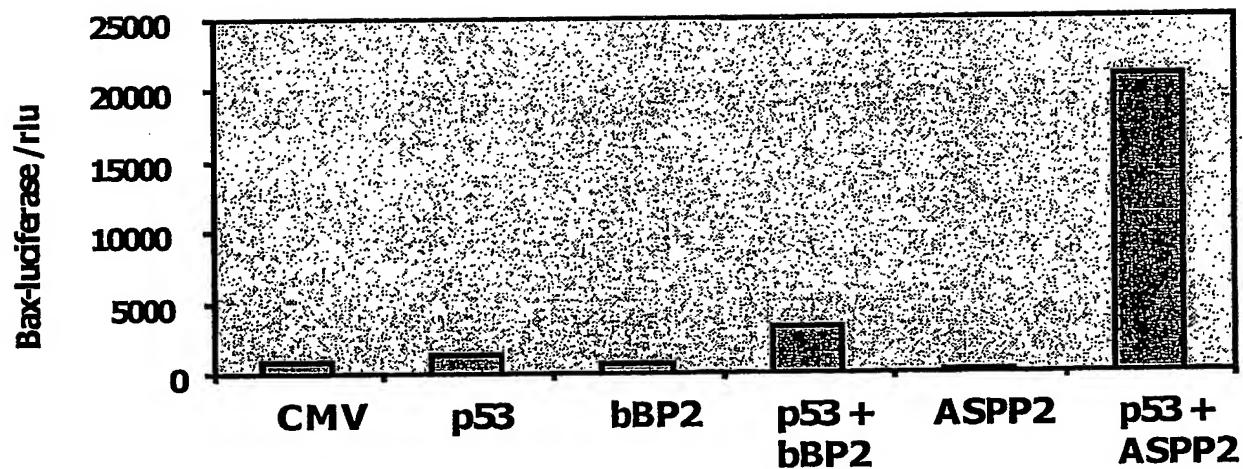
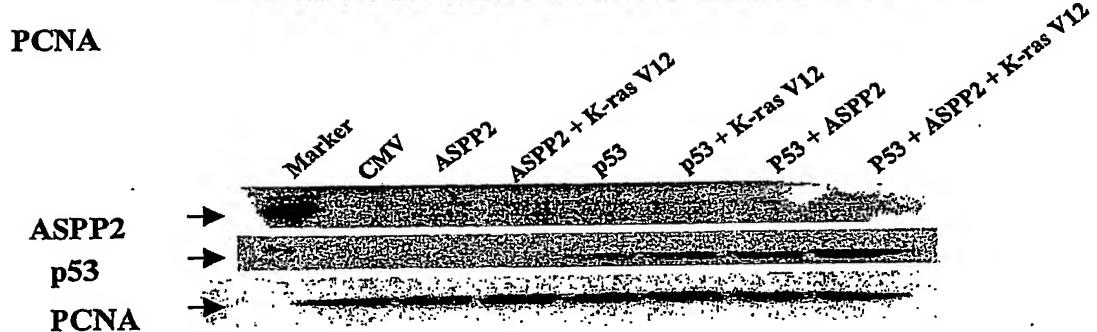
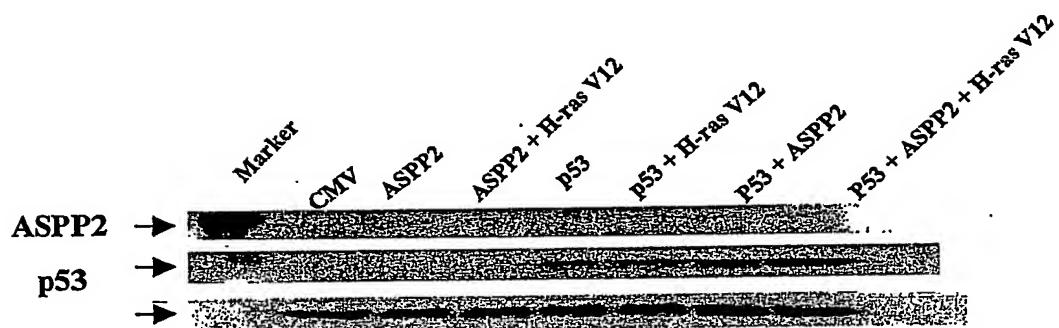
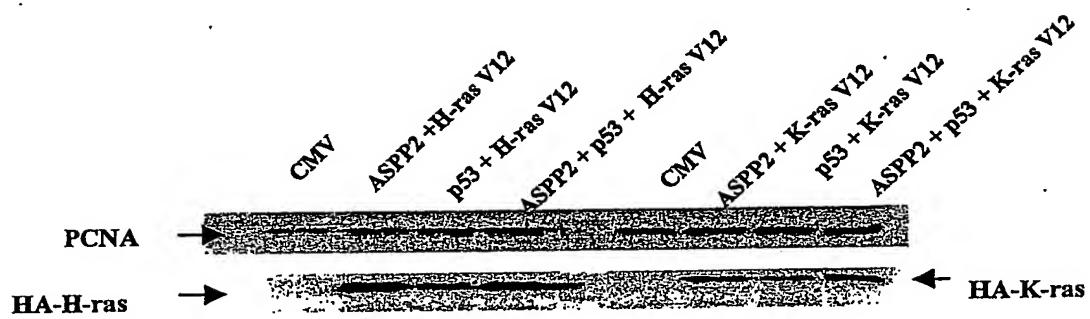
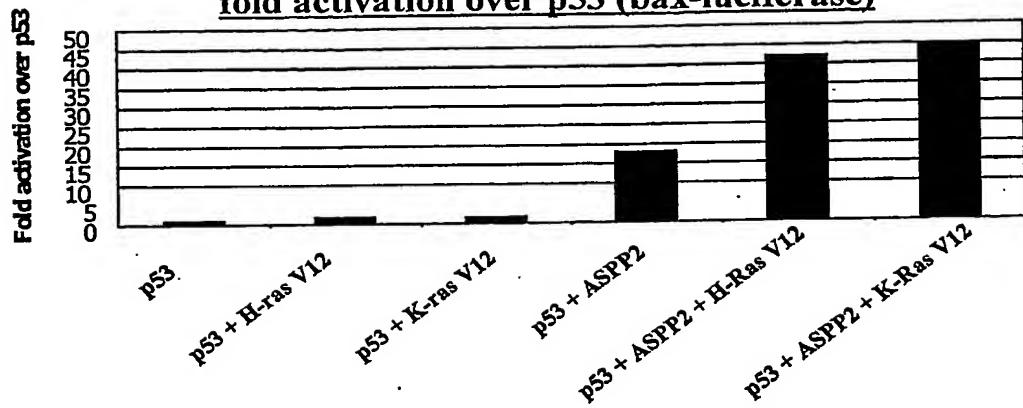


Figure 1: The N-terminal 130 amino acids of ASPP2 is crucial for its full activity

Fig 2

fold activation over p53 (bax-luciferase)



H-ras and K-ras activate ASPP equally

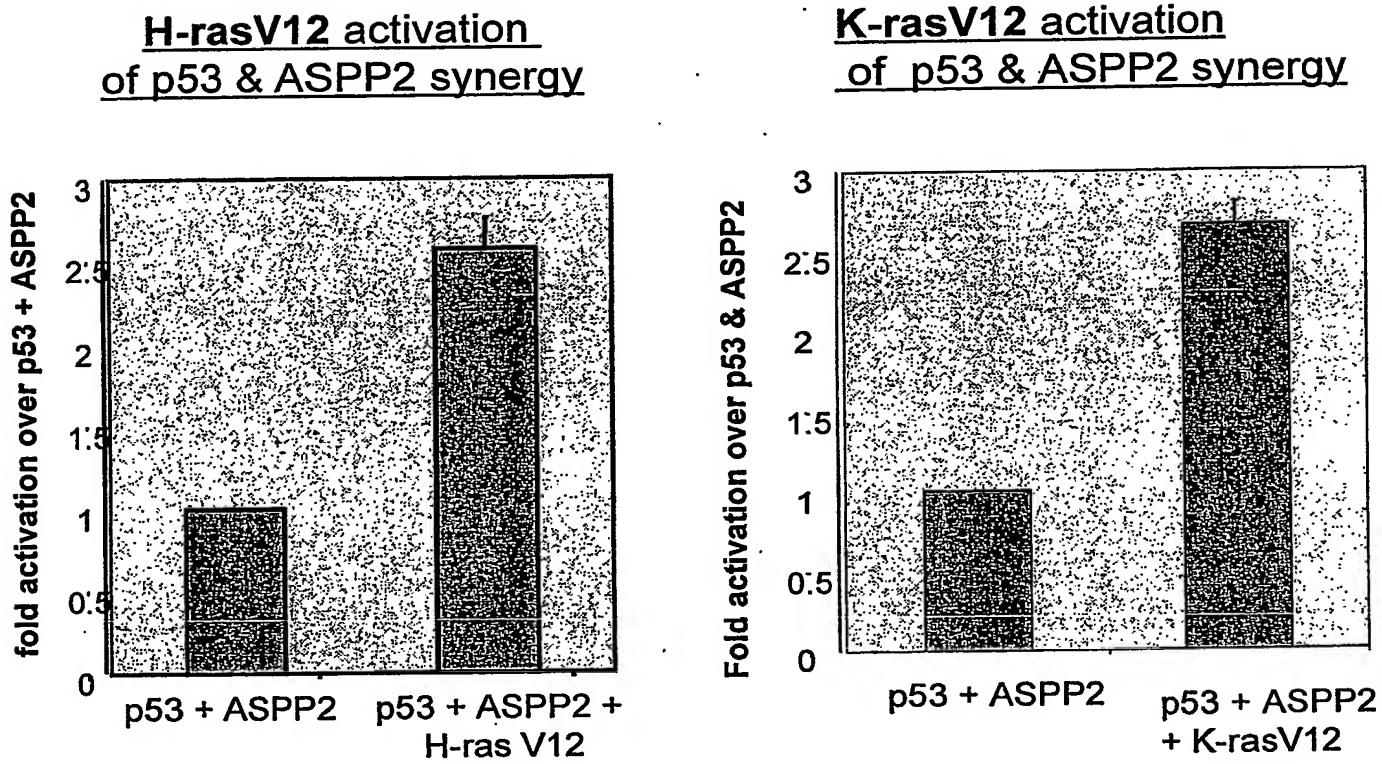


Figure 3:

Promoter specificity

Figure 4A

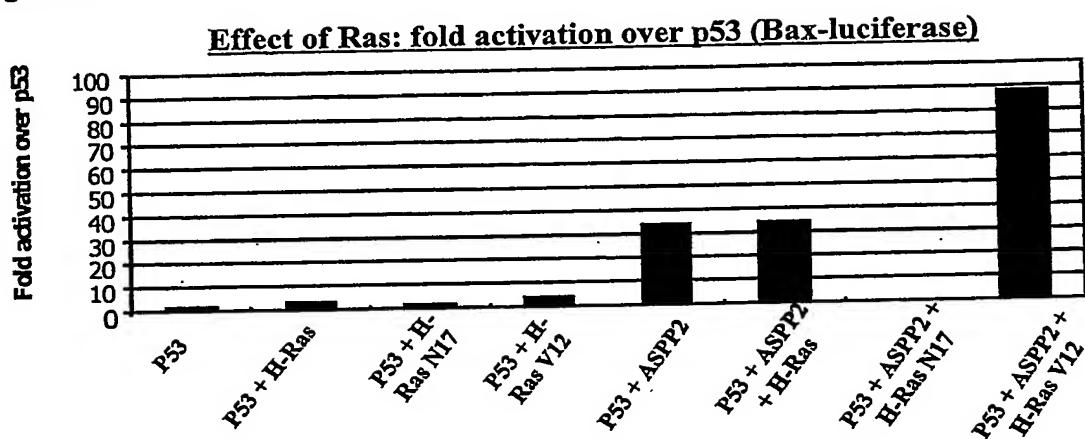


Figure 4B

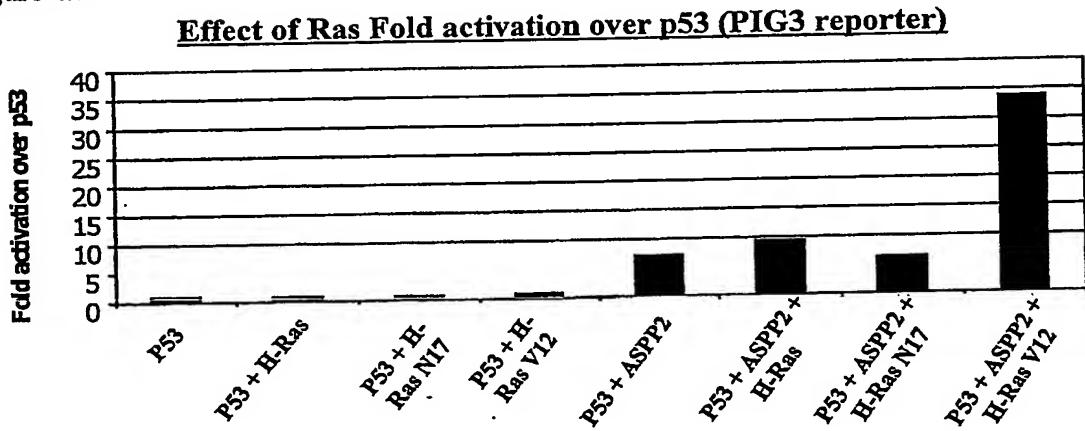


Figure 4C

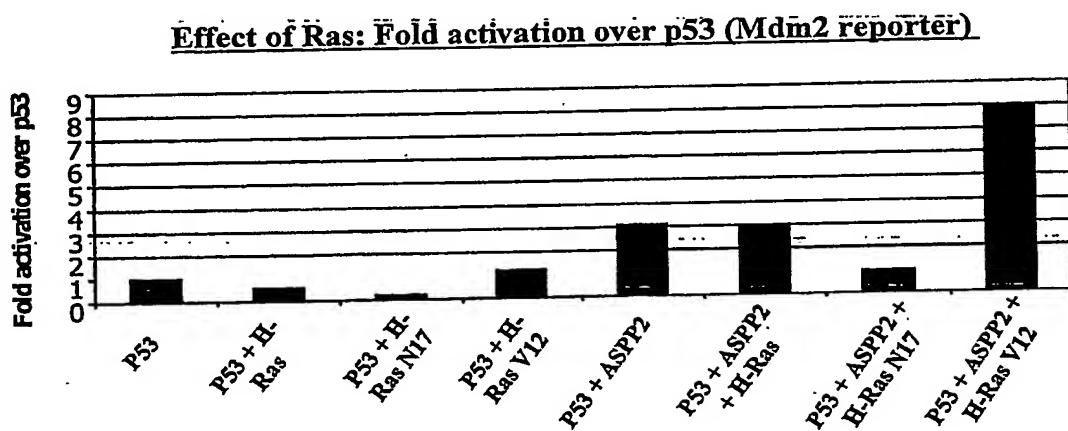


Figure 4D

Effect of rasV12 on transactivation: comparing three reporters

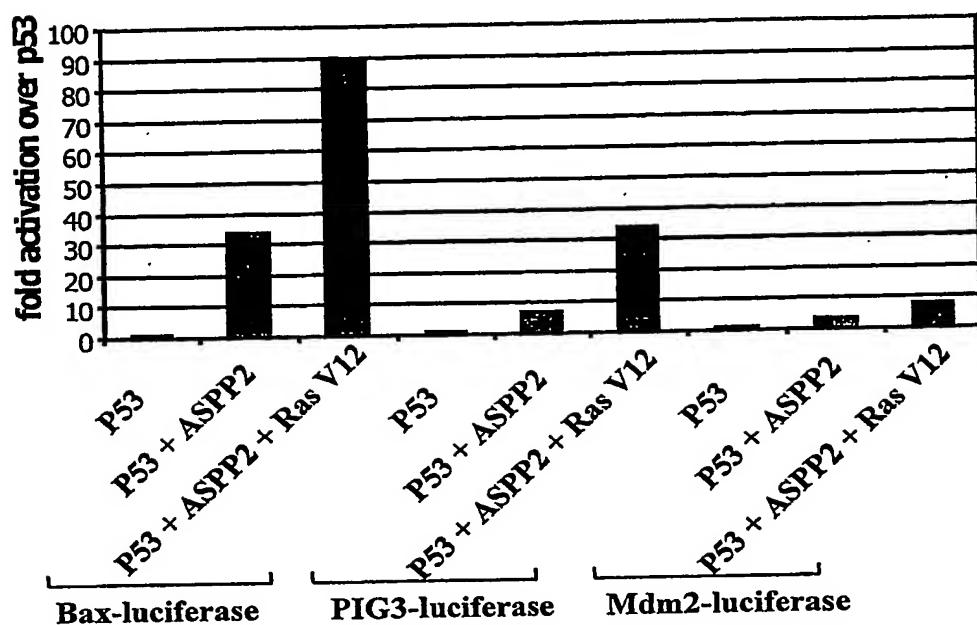


Figure 4E

Promoter specificity of rasV12

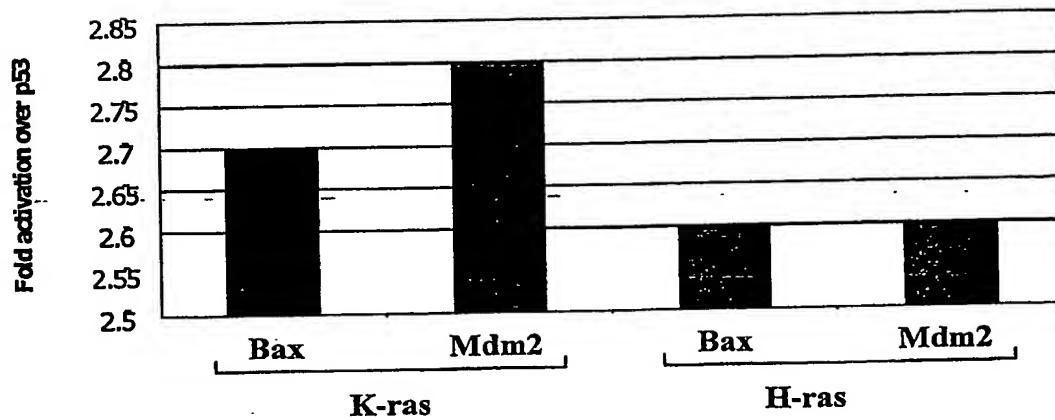


Figure 5A

H-rasV12 activates endogenous ASPP2 to transactivate bax reporter (U2OS cells)

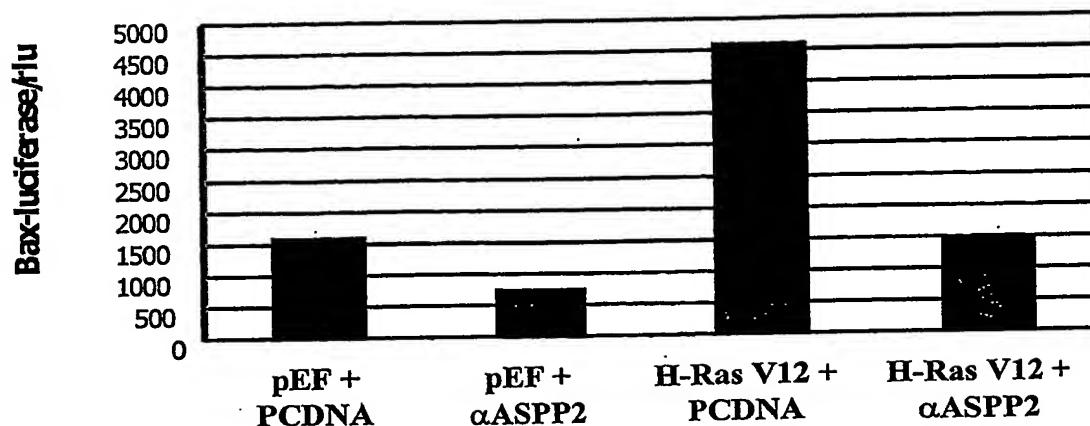
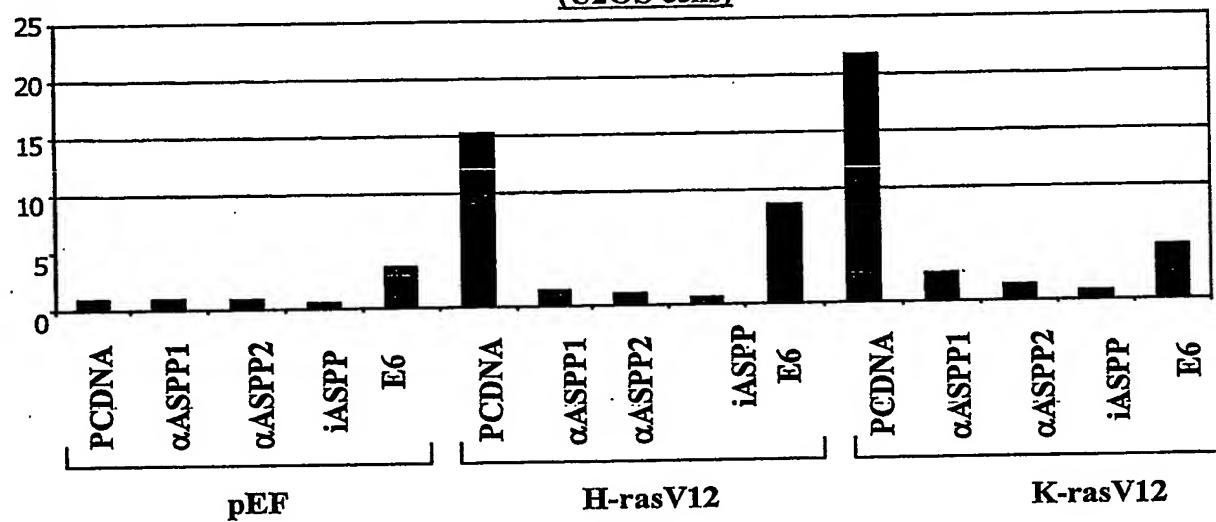


Figure 5B

H- and K-rasV12 activate endogenous ASPP1, ASPP2 and p53 to transactivate bax-reporter (U2OS cells)



Checking efficiency of Ras RNAi

Western blot analysis of HA-H-rasV12 and HA-K-rasV12 expression. The blot shows bands for HA-H-rasV12 (~21 kDa) and HA-K-rasV12 (~21 kDa) across various cell lines. Lanes are grouped by promoter: vector, H-ras pSUPPRESSOR, K-ras pSUPPRESSOR, H-ras pSUPER, and K-ras pSUPER. An arrow on the left points to HA-H-rasV12, and an arrow on the right points to HA-K-rasV12.

Fig 6A

Figure 6B

Effect of H/K-Ras pSUPER on ASPP2 and p53 synergy

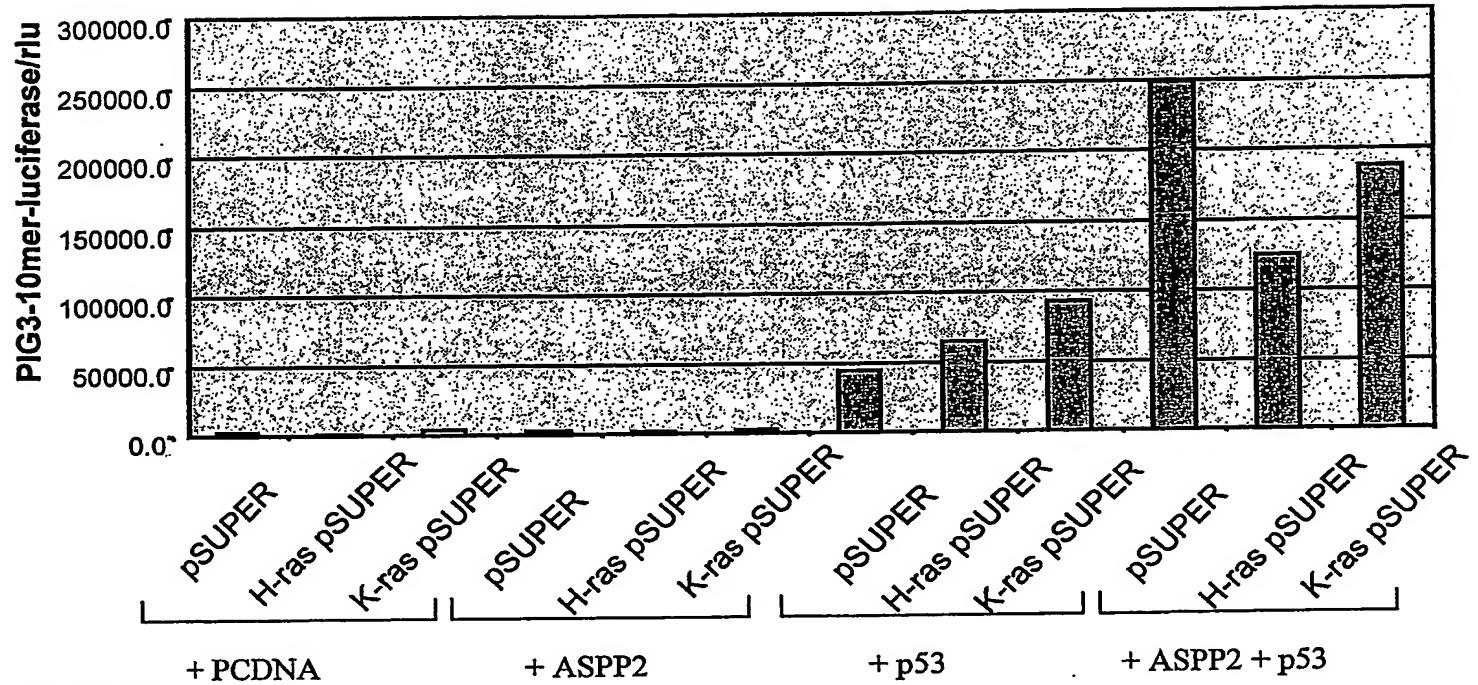
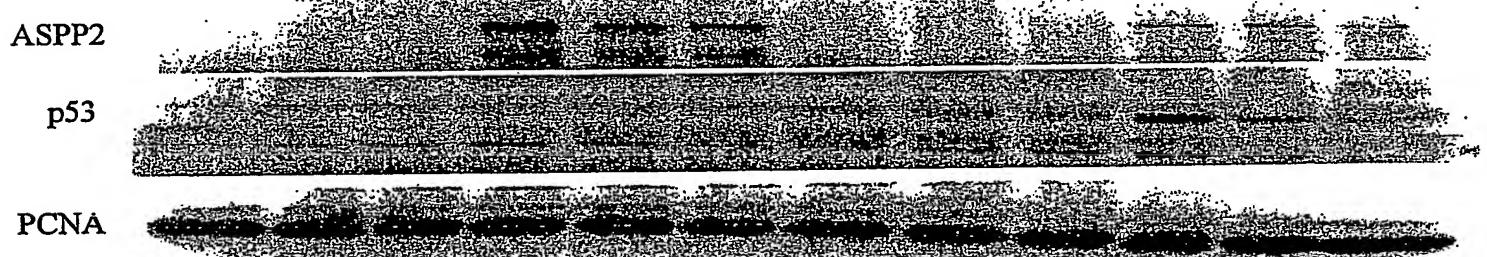


Figure 6C



Does Ras activate ASPP via its effector pathway?

Figure 7A: Effect of Ras and Raf CAAX: fold activation over P53 (Bax- reporter)

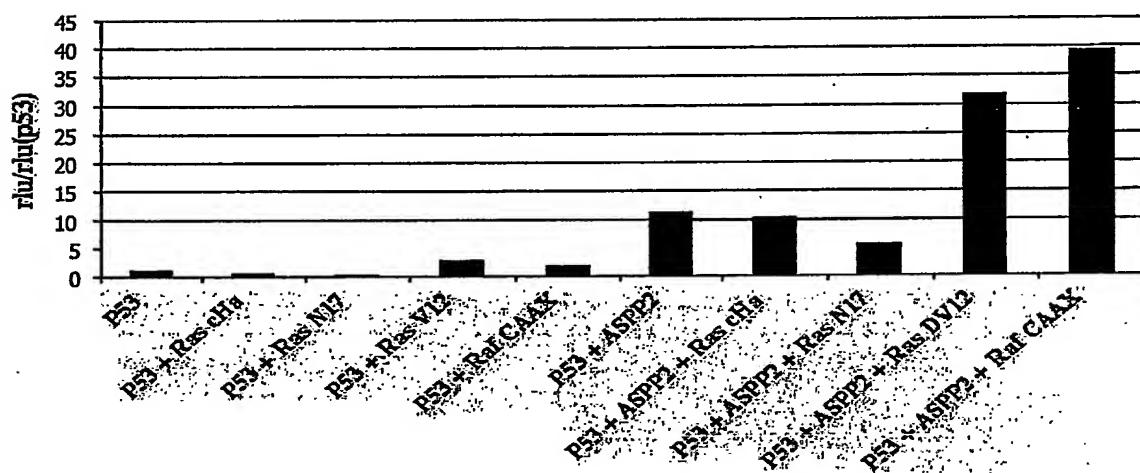


Figure 7B Effect of activated Raf CX on ASPP2 & p53 synergy

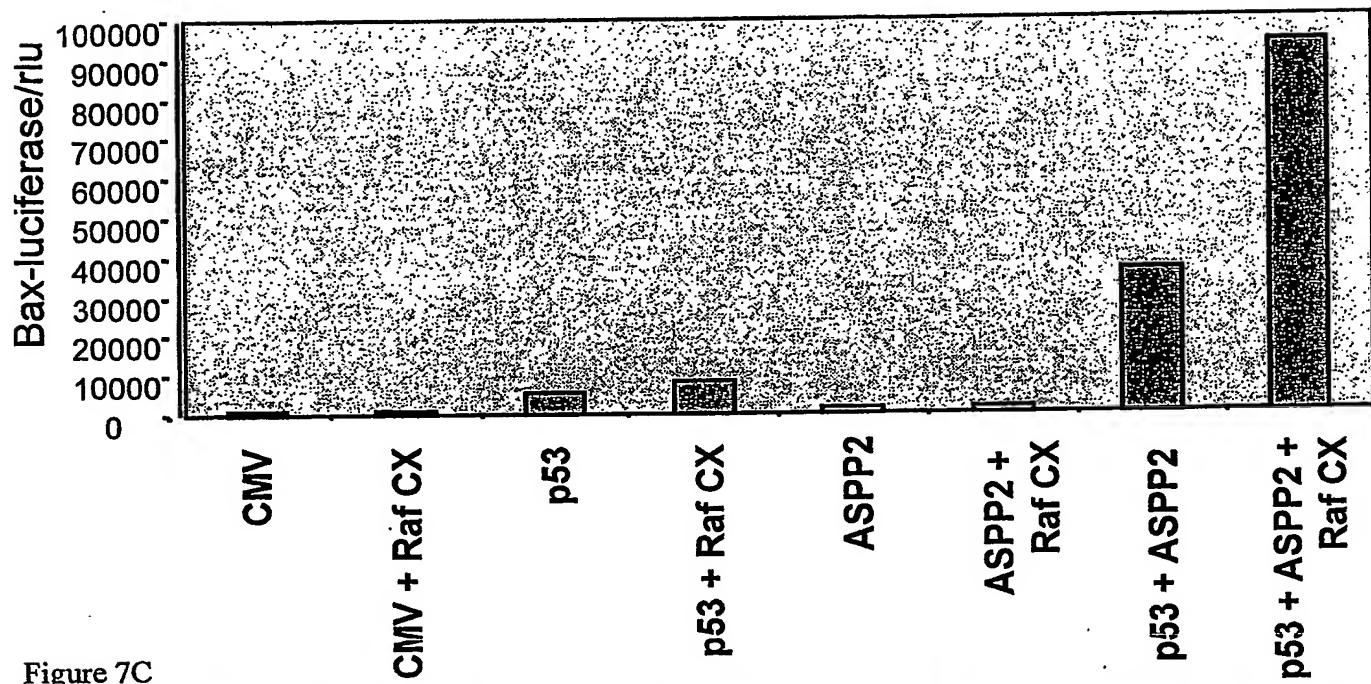
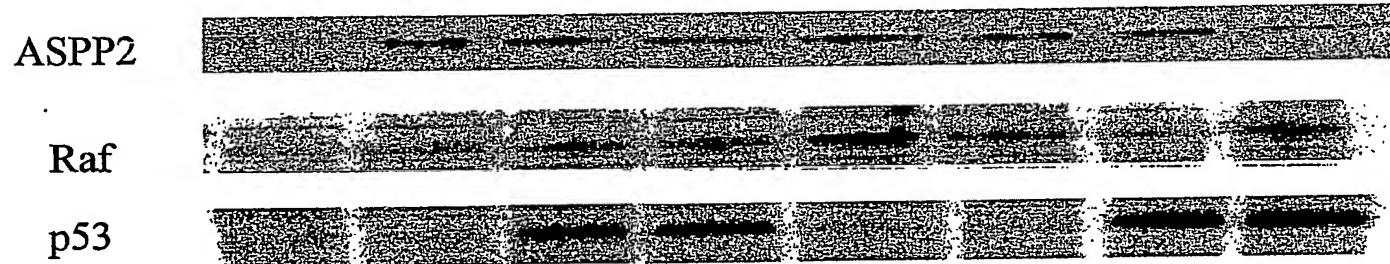
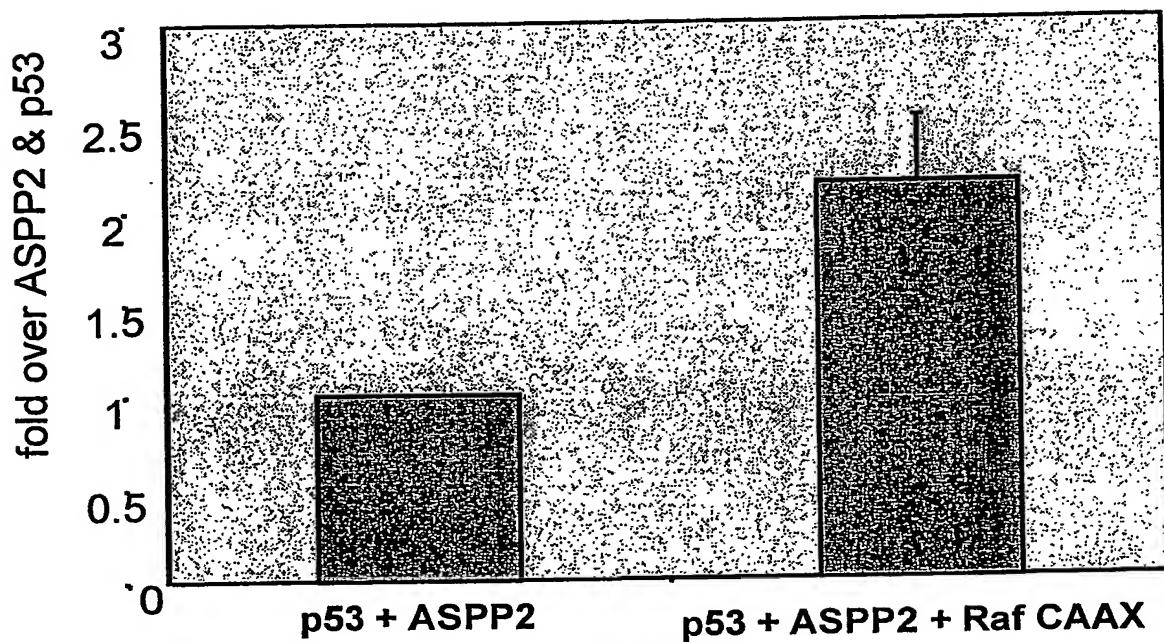


Figure 7C



Effect of RafCAAX on ASPP2 & p53 synergy
(bax-luciferase)



$f_{ij} \geq 0$

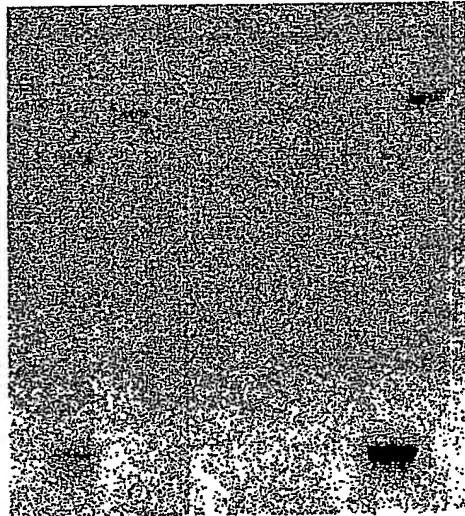
Figure 8A

MAPK1 p70S6K p90rsk

H2B
ASPP2

H2B
ASPP2

H2B
ASPP2



PKA PKB p38SAPK

H2B
ASPP2

PKB

H2B
ASPP2

p38SAPK

H2B
ASPP2

ASPP2

H2B

Figure 8B

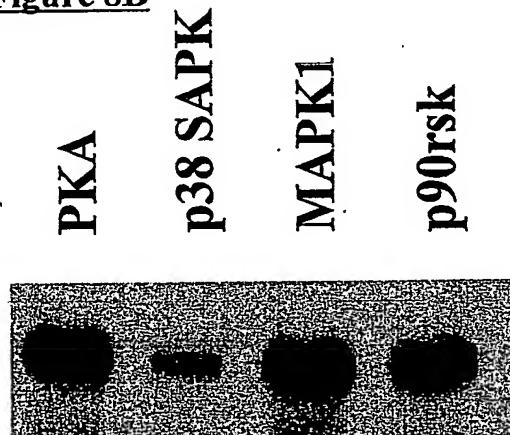


Figure 8C

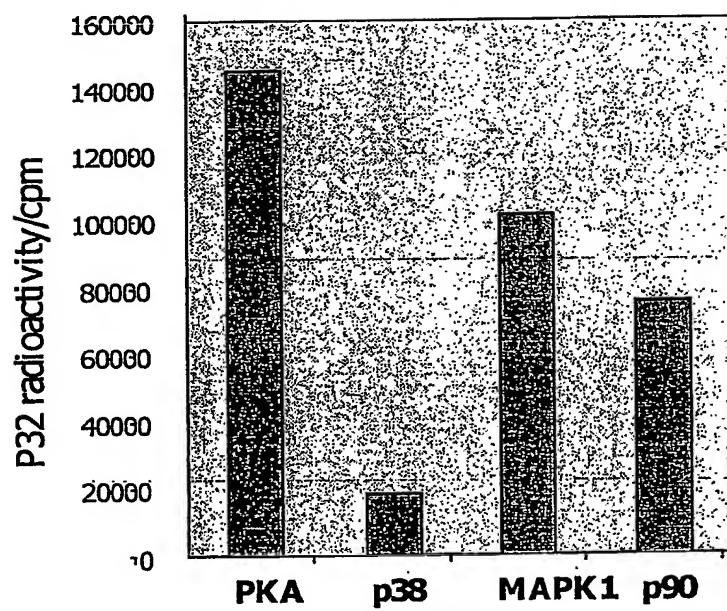
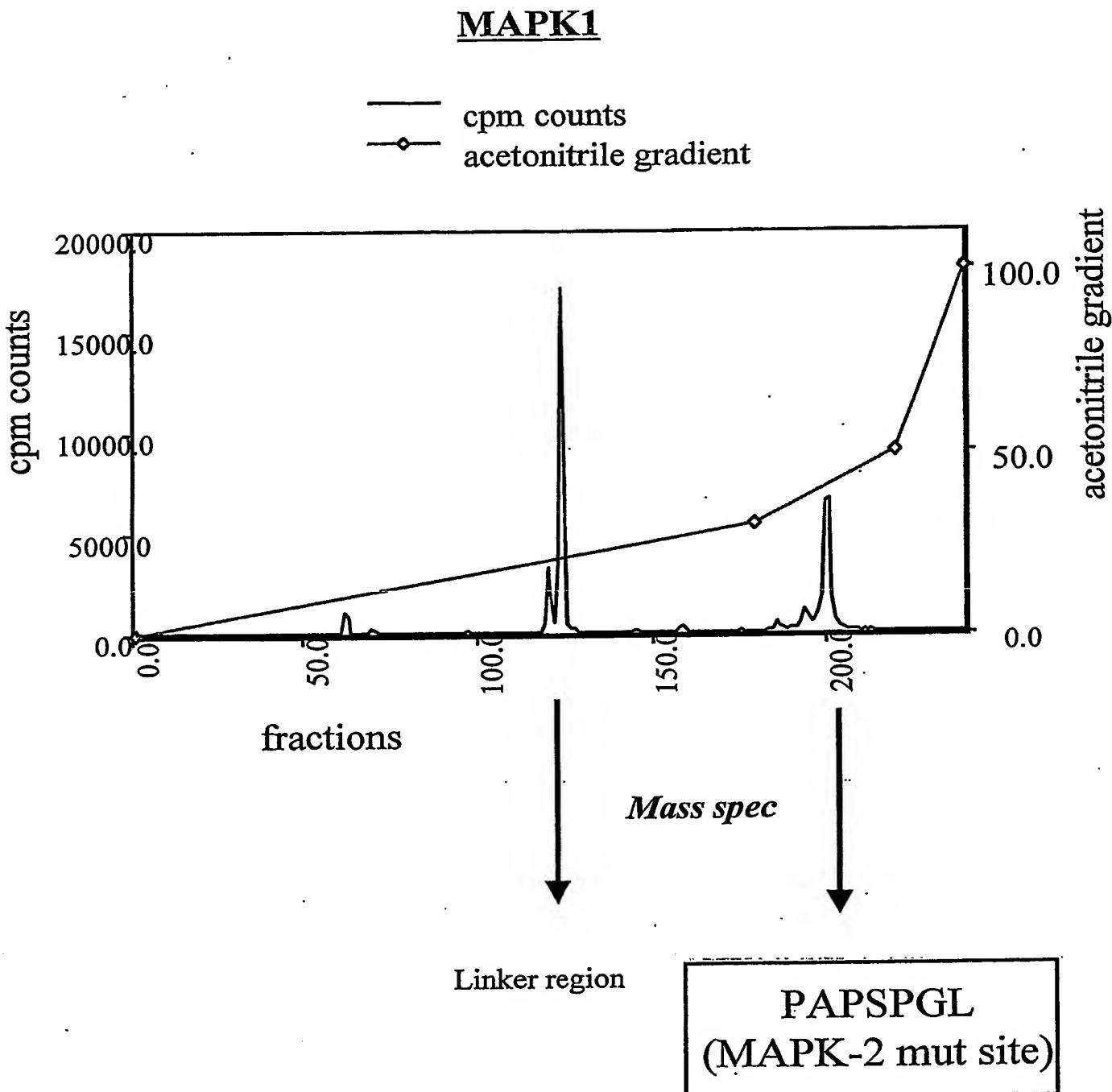


Figure 8D.



ASPP2 Mutants

C-term of ASPP2:

550 - QPRVLLSPSIPSVGQDQTLSPGSKQESPPAAA VRPFTPQPS
KDTLLPPFRKPQTV AASSIYSMYTQQQAPGKNFQQAVQS
ALT KTHTRGPHFSSVY GKPVIAAAQNQQQHPENIYSNSQ
GKPGSPEPETEPVSSVQENHENERIPRPLSPTKLLPFLSNP
YRNQSDADLEALRKKLSNAPRPLKKRSSITEPEGPNGPNI
QKLLYQRTTIAAMETSVPSYPSKSASVTASSESPVEIQNP
YLHVEPEKEVVSLVPESLSPEDVGNASTENSDMPAPSPGL
DYEPEGVPDNSPNLQNNPE - 849

S — MAPK sites
SS — PKA site

Fig 9

Figure 10A

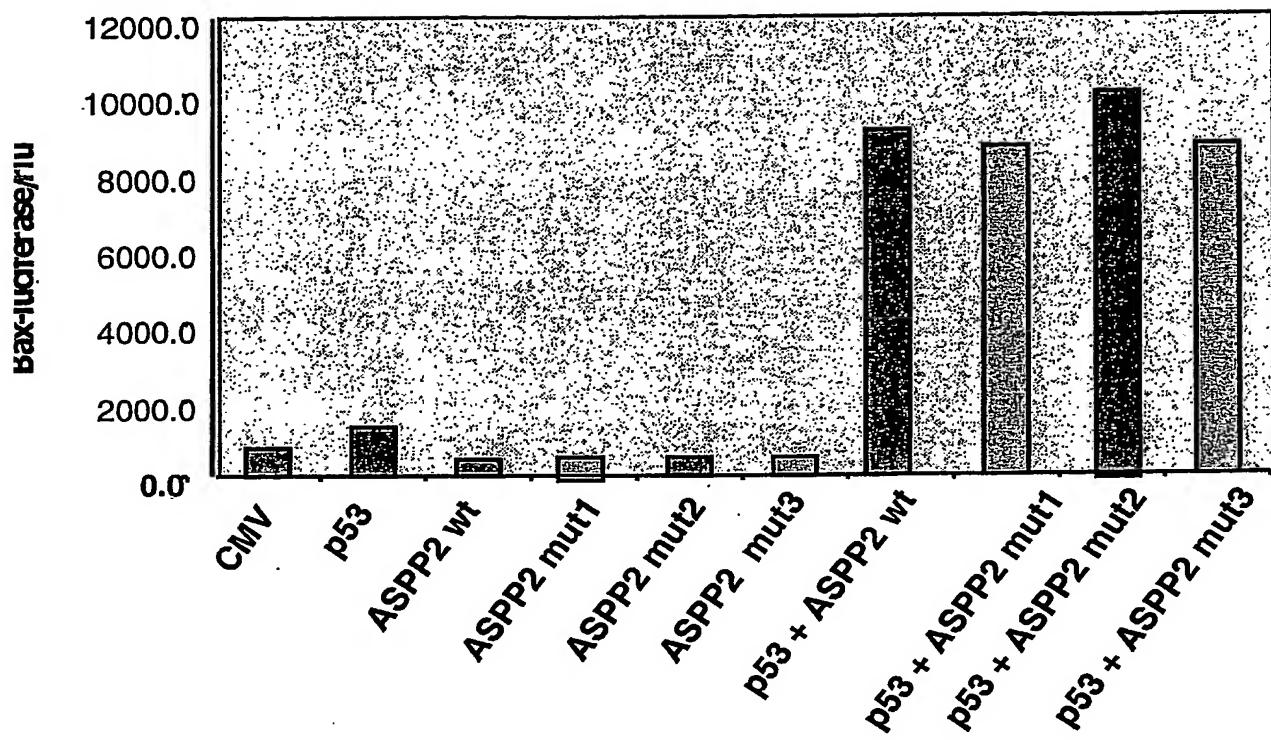


Figure 10B

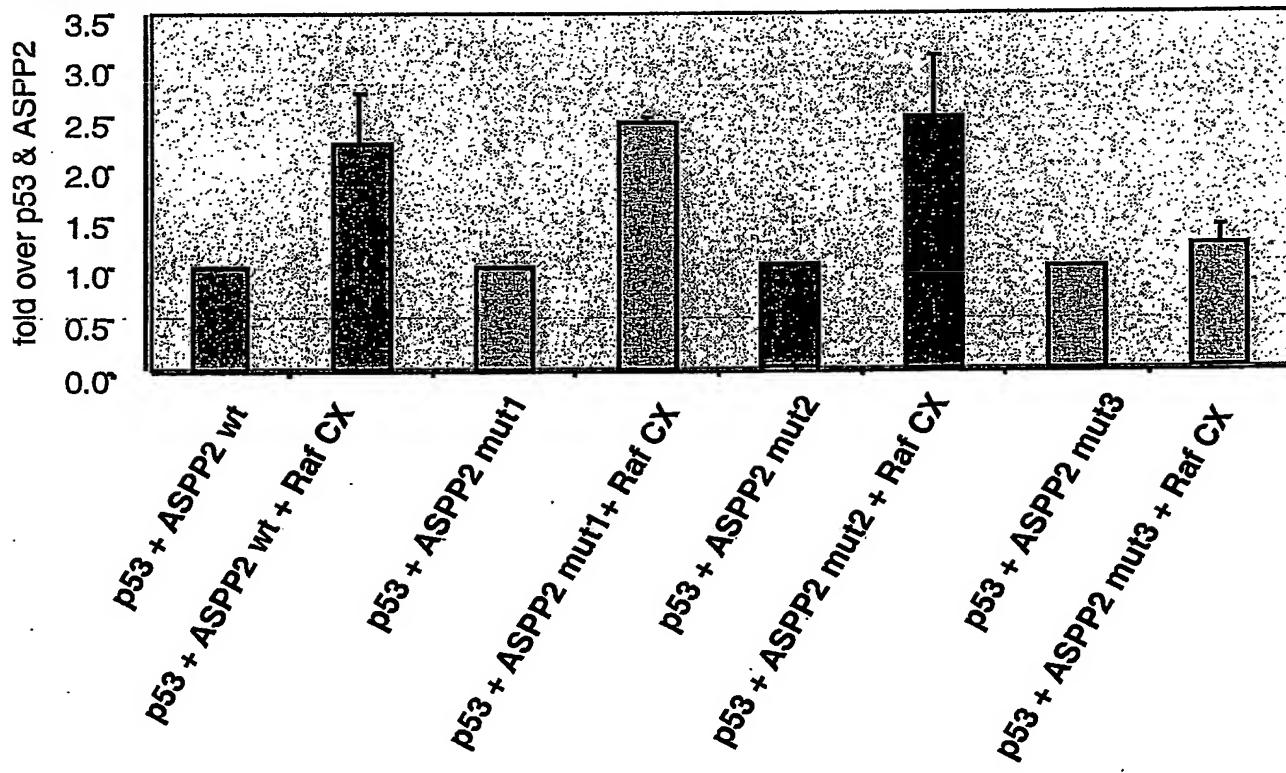


Figure 11A

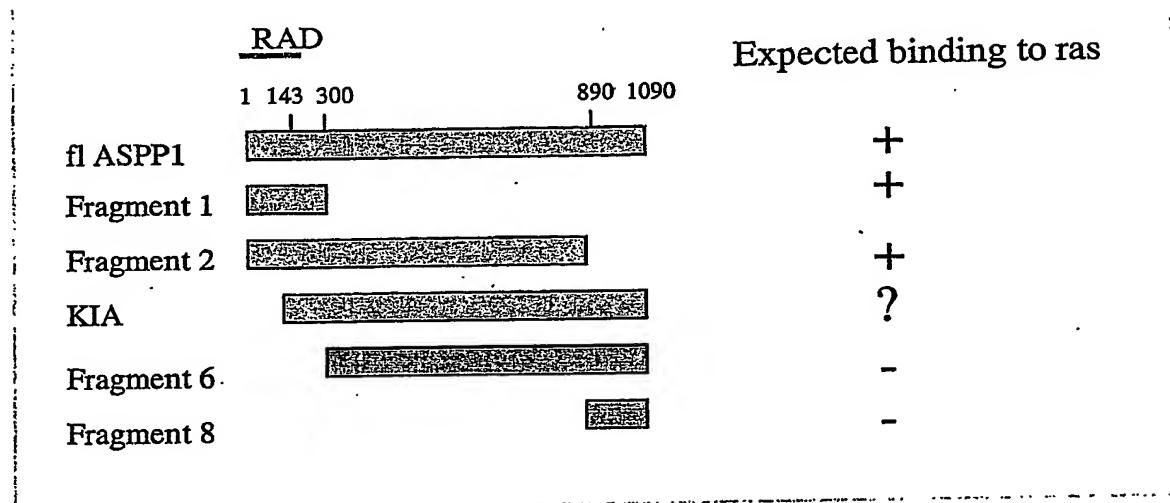
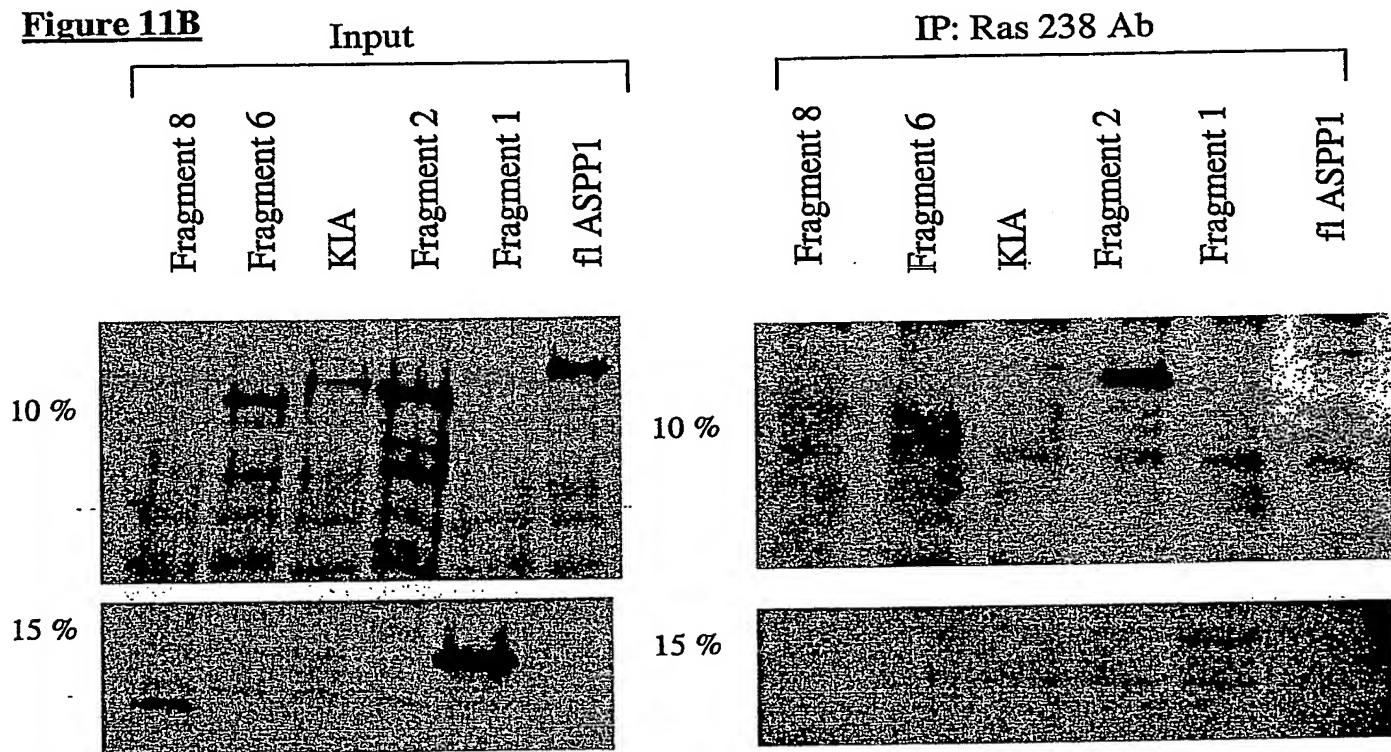


Figure 11B



Endogenous Ras binds ASPP2 after stimulation with EGF

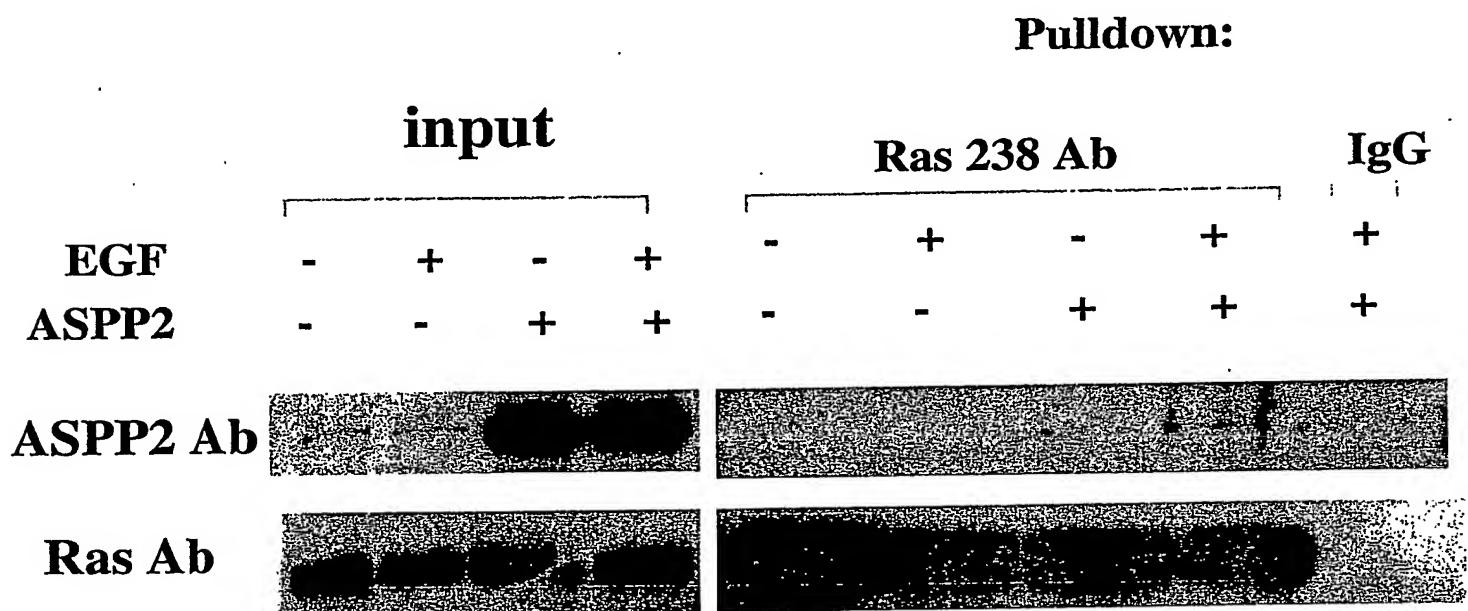


Fig 12

**Endogenous ASPP1 and ASPP2 bind endogenous Ras
after EGF and 20% FCS stimulation**

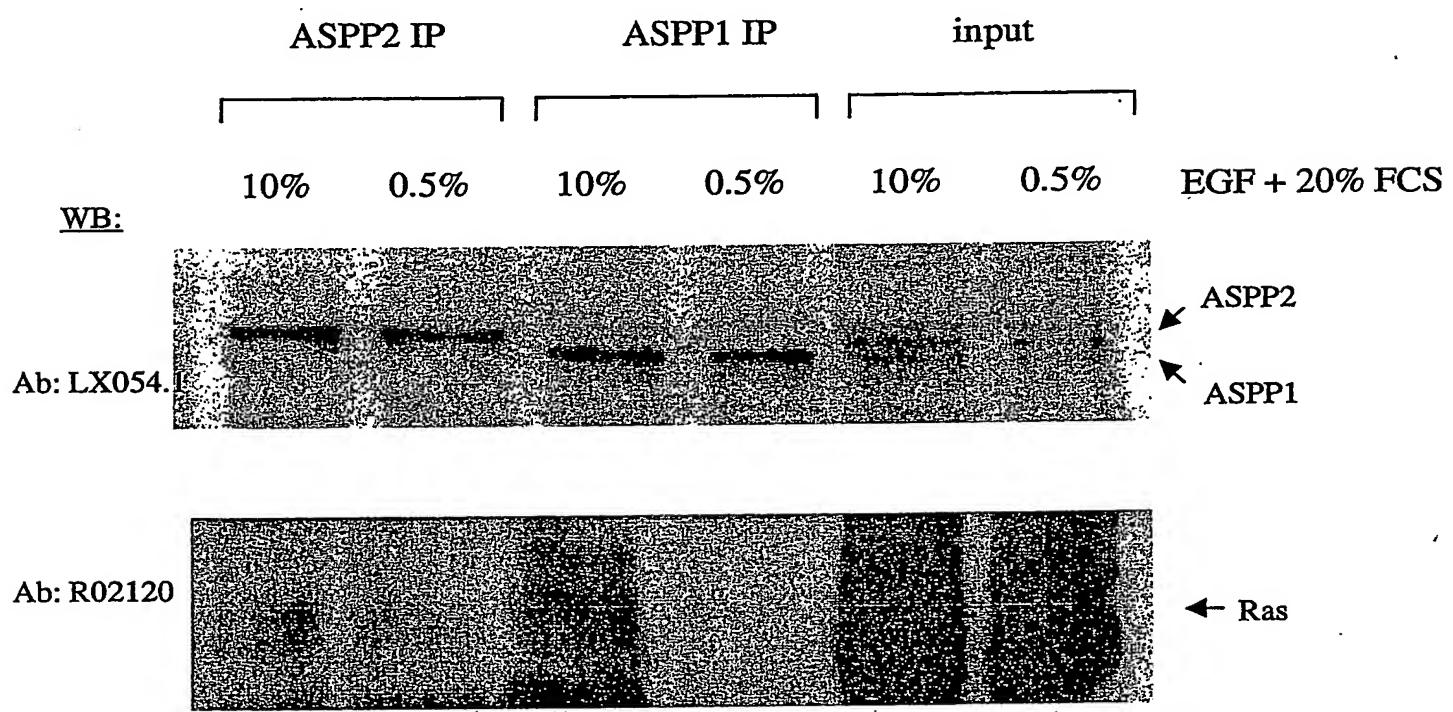


Figure 13

Figure 14A

Loading of Ras.GDP and Ras.GTP (cpm)

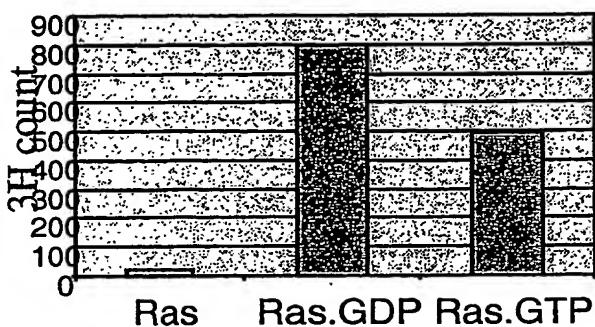


Figure 14C

input

N-term ASPP1 pulldown (V5)

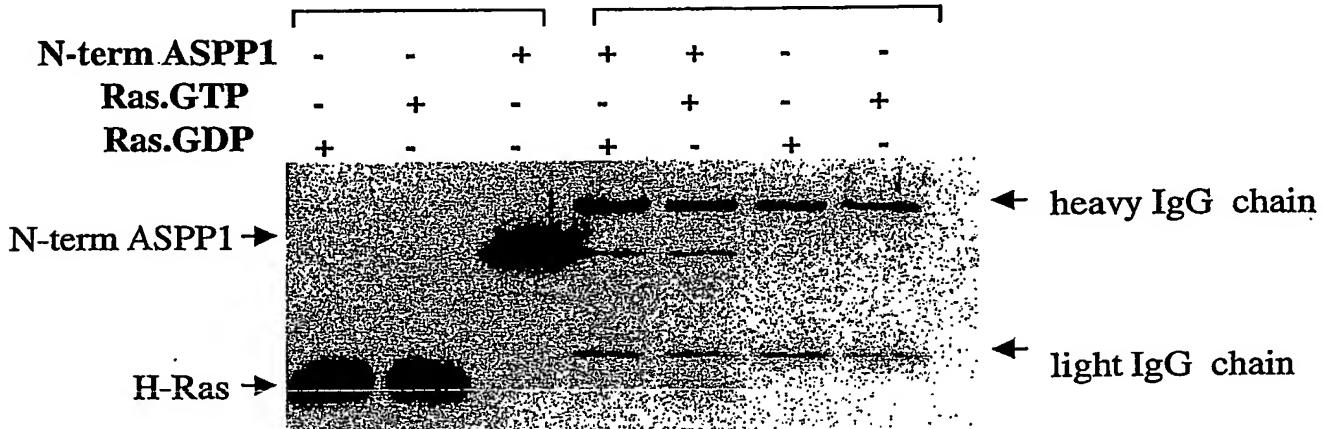
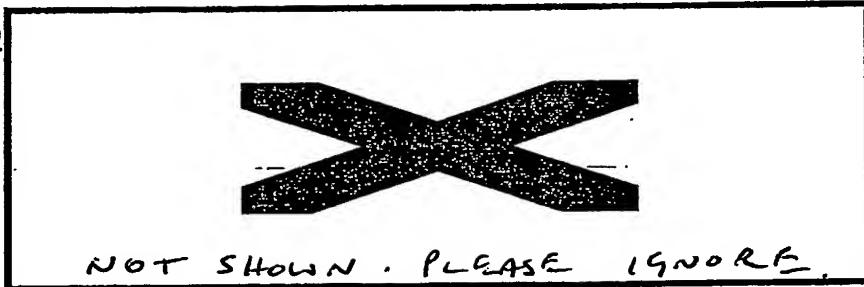


Figure 14D



ASPP2 + H-RasV12

ASPP2



ASPP2 + H-RasV12

H-RasV12



Merged

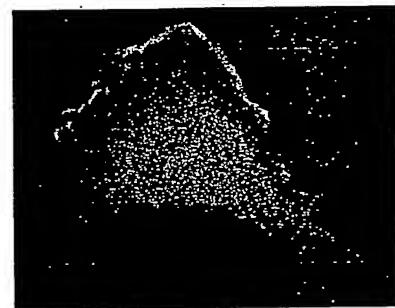


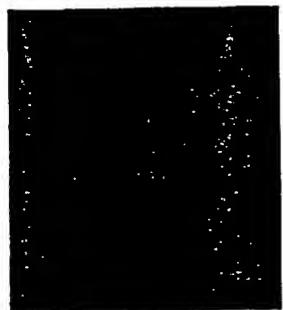
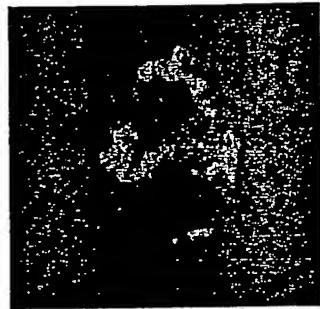
Fig 15

ASPP1

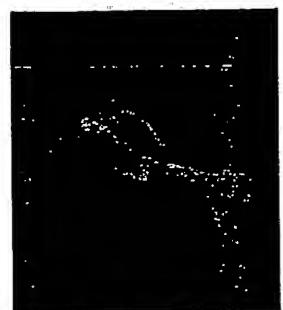
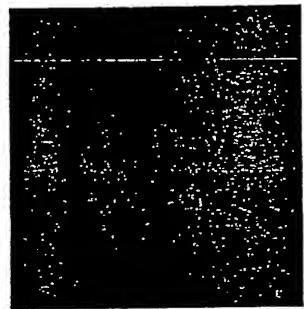
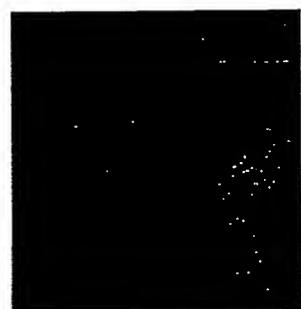
ASPP1 + K-ras V12

**ASPP1 + K-ras V1
+ UO126**

ASPP1



K-rasV12



Merged

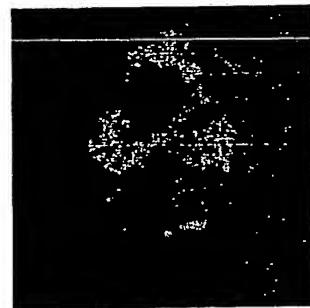


Fig 16

Figure 17a

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Figure 17b

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CT

Figure 17c

MMPLMILTVFLSNNEQILTEVPITPETTCRDUVEFCKEPGEGSCHLAEVWRGNERPIPFDHMMYEHLOQIWGPRREEVKFFLRHEDSPTEQSGRQTTQEQRTQRNVINVPGDKRTEYGVGNPRLTLESLQDMAARQQQIENQQQMLVAKERLHFLKQQERQQQSISENELQKLKERVEAQENKLKKIRAMRGQVDYSKIMGNLSAEIERFSAMFQEKKQBVQTAIRLVDQLSQQLEDLKKKGKLNQGFSYNGKLTGPAAVELKRLYQQLCIRNQLNQEONSKLQQQKELLNKRMEVAMMDKRISERLERYGKQIQLNRVNGTSSPQSLSTSGRVAAGVPIQVPSAGSFVLPDTPKQPSLISASNAAHGRSKSANDCNPTLKNQSSSSVKPVQVAGADWKDPSVGEVKSVQKGTVSQSPVPSALGPTKPGIEIGKVPPPIPGVKGQLPPSYGTVPSPTPLGPGSTSSLENRKEGSPLPRPSAGLFSRQRPRTLLPATGSTPQPGSSQQIQQRISVPPSPTYPPAGPPAFPAGDKSKPELPLTVAIRPFLADKGSRPQSPRKGPQTVNSSIYSMYLQQATPPKNYQPAAHSLNKSVAKYGKPVLPSTSPSPLPFLHGSLSLTGTQPQQPQPSSESTEKEPEQDQGPAAQADGSTVESLPRPLSPKLTPIVHSPLRYQSDADLEALRRKLANAPRPLKKRSSITEPEGPGGPNIQKLLYQRFNTLIAAGGMGCTPFYQPSPSQDFMCTLADVDNGNTNANGNLLEELPPAQPTALPAPAEPAFSSDANDNELPSPEEELICPQTTHQTAEPaedNNNNVATVPTTEQIPSPVNEAPSPGEEQVPPAPLPPSHAPATSTNKRNLKPPNSERTGHLGRFRFPNPLALLDASLEGEFDLVRQIYIEVEDPSKPNDEGITPLHNAVGCHHHITVKFLLDGVNVNAADSDGWTPLHCAASCNVSHLCKQLVSGAAIFFASTISDIETAAADKCEEMEEGYIQCQSFYLVGQEKLGVMNKGVAYALWDYEAQNSDELSFHEGDALTI LRRKDESETEWWWARLGDRREGYVPKNLLGLYPRIKPRQRTLA

Figure 17d

MMPMFVYLSSNEQHFTEVPTPETICRDVVVLCKEPGESDCHLAEVWCGSERPVADNERMFDVLRQFGSQRNEVRFFLRHIERPPGRDIVSGPRSQDPSLKRNGVKVPGHEYRRKBNGVNSPRMDLTIAELQEMASRQQQIEAQQQLLATKEQRLKFLKQQDQRQQQVAEQEKLKRLKEIAENQEAKLKKVRALKGHVEQKRLSNGKLVEEIEQMNLFQQKQRELVLAVSKVEELTRQLEMLKNGRIDSHHDNQSAVAEFLDRLYKELQLRNKLNEQNAKLQQQRECLNKRNEVAVMDKRVNELRDRLWKKAAALQOKENLPVSSDGNLPQQQASAPSRAAVGPYIQSSTMRMPSRPELLVVKPALPDGSLVIQASEGPMKIQTLPNMRSGAASQTKGSKIHPVGPDWSPSNADLFPSSQGSASVPQSTGNALDQVDDGEVPLREKEKKVRPFMSFDADVQDSNAPPSSFGTLRKKNQSSEDLRDAQVANKNVAKVFPVPTKPKQINLPYFGQTNQOPPSDIKPDGSSQQLSTVVPMSGTPKPKPAGQQPRVLLSPSIPSVGQDQTLSPGSKQESPPAAAVRPFTPQPSKDTLLPFRKPQTVAASSIYSMYTQQQAPGKNFQQAVQSAITKTHTRGPHFSSVYGPVIAAAQNQQQHPENIYSNSQGKPGSPEPEPEPVSSVQENHENERIPRPLSPTKLLPFLSNPYRNQSDADLEA LRKKLISNAPRPLKKRSSITEPEGPNGPNIQKLLYQRTTIAAMETISVPSYPSKSASVTASSESPVEIQNPYLHVEPEKEV VSLVPESLSPEDVGNASTENSDMPAPSPGLDYEPGVPDNSPNLQNNPEEPNPAPHVLDVYLEEYPPVPPPPPSGEPE GPGEDSVSMRPEITGQVSLPPGKRTNLRKTGSERIAHGMRVKFNPLALLLDSSLEGEFDLVQRRIIYEVDDPSLPNDEGI TALHNAVCAGHTEIVKFLVQFGVNVNAADSDGWTPLHCAASCNNQVCKFLVESGAAVFAMTYSDMQTAADKCEEMEEGY TQCSQFLYGVQEKGIMNKGVIALWDYEPQNDDELPKEGDCMTIIHREDEDEIEWWWARLNDKEGYVPRNLLGLYPRI KPRQRSLA

H-ras wild type DNA

Figure 18a

ATGACGGAATATAAGCTGGTGGTGGTGGCGCCGGCGGTGTGGGCAAGA
GTGCGCTGACCATCCAGCTGATCCAGAACCATTTGTGGACGAATACGAC
CCCACTATAGAGGATTCTACCGGAAGCAGGTGGTCATTGATGGGGAGAC
GTGCCTGTTGGACATCCTGGATACCGCCGGCCAGGAGGAGTACAGCGCCA
TGCAGGACCAACTACATGCGCACCGGGGAGGGCTTCTGTGTGTGTTGCC
ATCAACAACACCAAGTCTTGAGGACATCCACCAAGTACAGGGAGCAGAT
CAAACGGGTGAAGGACTCGGATGACGTGCCATGGTGCTGGTGGGAAC
AAGTGTGACCTGGCTGCACGCACGTGGAATCTCGGCAGGCTCAGGACCT
CGCCCGAAGCTACGGCATCCCCATCGAGACCTCGGCCAAGACCCGGC
AGGGAGTGGAGGATGCCTTACACGTTGGTGCAGATCCGGCAGCAC
AAGCTGCGGAAGCTGAACCCCTCTGATGAGAGTGGCCCCGGCTGCATGAG
CTGCAAGTGTGTGCTCTCCTGA

Figure 18b

MTEYKLVVVGAGGVGKSALTIQLIQNHFVDEYDPTIEDSYRKQVVIDGETCL
LDILDTAGQEEYSAMRDQYMRTGEGFLCVFAINNTKSFEDIHQYREQIKRVK
DSDDVPMVLVGNKCDLAARTVESRQAQDLARSYGYIETSAKTRQGVEDA
YTLVREIRQHKLRLKNPPDESGPGCMSCKCVLS

H-ras oncogenic DNA

Figure 18c

ATGACGGAATATAAGCTGGTGGTGGGCGCCGTCGGTGTGGGCAAGA
GTGCGCTGACCATCCAGCTGATCCAGAACATTGTGGACGAATACGAC
CCCACATAGAGGATTCCTACCGGAAGCAGGTGGTATTGATGGGGAGAC
GTGCCTGTTGGACATCCTGGATACCGCCGGCAGGAGGAGTACAGCGCCA
TGCAGGACCAACTACATGCGACCCGGGAGGGCTTCCTGTGTGTGTTGCC
ATCAACAAACACCAAGTCTTGAGGACATCCACCAAGTACAGGGAGCAGAT
CAAACGGGTGAAGGACTCGGATGACGTGCCCATGGTGTGGTGGGAAC
AAGTGTGACCTGGCTGCACGCACTGTGGAATCTCGGCAGGCTCAGGACCT
CGCCCCGAAGCTACGGCATCCCTACATCGAGACCTCGGCCAAGACCCGGC
AGGGAGTGGAGGATGCCTCTACACGTTGGTGCCTGAGATCCGGCAGCAC
AAGCTGCGGAAGCTGAACCCCTGATGAGAGTGGCCCCGGCTGCATGAG
CTGCAAGTGTGTGCTCCTGA

Figure 18d

MTEYKLVVVGAVGVGKSALTIQLIQNHFVDEYDPTIEDSYRKQVVIDGETCL
LDILDTAGQEEYSAMRDQYMRTGEGFLCVFAINNTKSFEDIHQYREQIKRVK
DSDDVPMVLVGNKCDLAARTVESRQAQDLARSYGIPYIETSAKTRQGVEDAF
YTLVREIRQHKLRLNPPDESGPGCMSCKCVLS-

K ras 4B wild type DNA

Figure 18e

ATGACTGAATATAAAGCTTGTGGTAGTGGAGCTGGTGGCGTAGGCAAGAG
TGCCTTGACGATACAGCTAATTCAAATCAGAATCATTGTGGACGAATATGATCC
AACAAATAGAGGATTCTACAGGAAGCAAGTAGTAATTGATGGAGAAACC
TGTCTCTGGATATTCTGACACAGCAGGTCAAGAGGGAGTACAGTGCAAT
GAGGGACCAGTACATGAGGACTGGGGAGGGCTTCTTGTGTATTGCCA
TAAATAATACTAAATCATTGAAGATATTCAACCATTATAGAGAACAAATT
AAAAGAGTTAAGGACTCTGAAGATGTACCTATGGTCCTAGTAGGAAATAA
ATGTGATTTGCCTCTAGAACAGTAGACACACAAAACAGGCTCAGGACTTAG
CAAGAAGTTATGGAATTCTTTATTGAAACATCAGCAAAGACAAGACAG
GGTGTGATGATGCCTCTATACATTAGTTGAGAAATTGAAAACATAA
AGAAAAGATGAGCAAAGATGGTAAAAAGAAGAAAAAGAAGTCAAAGAC
AAAGTGTGTAATTATGTAA

Figure 18f

MTEYKLVVVGAGGVGKSALTIQLIQNHFVDEYDPTIEDSYRKQVVIDGETCL
LDILDTAGQEEYSAMRDQYMRTGEGFLCVFAINNTKSFEDIHYREQIKRVK
DSEDVPMVLVGNKCDLPSRTVDTKQAQDLARSYGIPFIETSAKTRQGVDDAF
YTLVREIRKHKEKMSKDGKKKKKSKTKCIVIM-

K-ras 4B oncogenic DNA

Figure 18g

ATGACTGAATATAAACTTGTGGTAGTTGGAGCTGTCGGCGTAGGCAAGAG
TGCCTTGACGATACTACAGCTAATTCTAGAACATTCATTGTGGACGAATATGATCC
AACAAATAGAGGATTCTACAGGAAGCAAGTAGTAATTGATGGAGAAACC
TGTCTCTGGATATTCTCGACACACAGCAGGTCAAGAGGGAGTACAGTGCAAT
GAGGGACCACTACATGAGGACTGGGGAGGGCTTCTTGTGTATTGCCA
TAAATAATACTAAATCATTTGAAGATATTCACTTATAGAGAACAAATT
AAAAGAGTTAAGGACTCTGAAGATGTACCTATGGTCTTAGTAGGAAATAA
ATGTGATTGCCTCTAGAACAGTAGACACACAAAACAGGCTCAGGACTTAG
CAAGAAAGTTATGGAATTCTTTATTGAAACATCAGCAAAGACAAGACAG
GGTGTGATGATGCCTCTATACATTAGTCGAGAAATTGAAAACATAA
AGAAAAGATGAGCAAAGATGGTAAAAAGAAGAAAAAGAAGTCAAAGAC
AAAGTGTGTAATTATGTAA

Figure 18h

MTEYKLVVVGAVGVGKSALTIQLIQNHFVDEYDPTIEDSYRKQVVIDGETCL
LDILDTAGQEEYSAMRDQYMRTGEGFLCVFAINNTKSFEDIHYREQIKRVK
DSEDVPMVLVGNKCDLPSRTVDTKQAQDLARSYGIPFIETSAKTRQGVDDAF
YTLVREIRKHKEKMSKDGGKKKKKSHTKCVIM-

Figure 19a

atggcggcgg cggcggcggc gggcggcggc ccggagatgg tccgcgggca ggtgttcgac
gtggggccgc gctacaccaa cctctcgac atcggcgagg gcgcctacgg catggtgtgc
tctgctttagt ataatgtcaa caaagttcga gtagctatca agaaaatcag ccccttttag
caccagaccc actgcccagag aaccctgagg gagataaaaaa tcttactgcg cttcagacat
gagaacatca ttggaatcaa tgacattttt cgagcaccaa ccatcggagca aatgaaaagat
gtatataatag tacaggaccc catggaaaca gatcttaca agctcttcaa gacacaacac
ctcagcaatg accatatactg ctattttctc taccagatcc tcagagggtt aaaatataatc
cattcagcta acgttctgca ccgtgaccc aacccttcca acctgctgct caacaccacc
tgtatctca agatctgtga ctggccctg gcccgttgc cagatccaga ccatgatcac
acagggttcc tgacagaata tggccaca cgttggtaca gggctccaga aattatgtg
aattccaagg gctacaccaa gtccattgtt atttggtctg taggctgcat tctggcagaa
atgcttctca acaggcccatttccagg aaggcattatc ttgaccagct gaaacacatt
ttgggtattt ttggatcccc atcacaagaa gactgaaatt gtataataaa tttaaaaagct
aggaactatt tgctttctct tccacacaaa aataagggtgc catggaaacag gctgttccca
aatgctgact ccaaagctct ggacttattt gacaaaatgt tgacattcaa cccacacaag
aggattgaag tagaacaggc tctggccac ccatactgg agcagtttta cgaccggagt
gacgagccca tcgccgaagc accattcaag ttgcacatgg aattggatga cttgcctaag
aaaaagctca aagaactaat ttgtaaagag actgcttagat tccagccagg atacagatct
taa

Figure 19b

MAAAAAAGAGPEMVRGQVFDVGPRYTNLSYIGEGAYGMVCSAYD
NVNKVRVAIKKISPFEHQTYCQRTLREIKILLRFRHENIIGINDIIRAPTEQMKDVKY
IVQDLMETDLYKLLKTQHLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLL
NTTCDLKICDFGLARVADPDHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDI
WSVGCILAEMLSNRPPIFFGKHYLDQLKHILGILGSPSQEDLNCIINLKARNYLLSLP
HKNKVPWNRLFPNADSKALDLKDMLTFNPHKRIEVEQALAHPYLEQYYDPSD
EPIAEAPFKFDMELDDLPKEKLKELIFEETARFQPGYRS

Figure 20a

1 tcgggctgag gttccggggc gggcgccgc ggagagacgc gggaaagcagg ggctggcg 61 gggtcgccgc gcccagcta gcgcagccag cccgagggcc gccgcgcgc cccgcgcg 121 cgctccgggg ccgcgcgcg cagccagcac ccgcgcgcg gcagctccgg gaccggcccc 181 ggccgcgcgc gccgcgtgg gcaacgcgcg cgccgcgaag aaggcagcg agcaggagag 241 cgtaaaagaa ttcttagcca aagccaaaga agatttctt aaaaaatggg aaagtcccgc 301 tcagaacaca gcccacttgg atcagttga acgaatcaag accctcgca cgggctcctt 361 cgggcgggtg atgctggta aacacaagga gaccgggaac cactatgcca tgaagatcct 421 cgacaaacag aagggtggta aactgaaaca gatcaacac accctgaatg aaaagcgcac 481 cctgcaagct gtcaacttgc cgttcctcgta caaactcgag ttctccttca aggacaactc 541 aaacttatac atggtcatgg agtacgtgcc cggcggggag atgttctcac acctacggcg 601 gatcggaaagg ttcaagtggc cccatgccc tttctacgcg gcccagatcg tcctgacctt 661 tgagtatctg cactcgctgg atctcatcta cagggacctg aagccggaga atctgctcat 721 tgaccagcag ggctacattc aggtgacaga cttcggttgc gccaagcgcg tgaagggccg 781 cacttggacc ttgtcgccgca cccctgagta cttggccctt gagattatcc tgagcaaagg 841 ctacaacaag gccgtggact ggtggccctt ggggggttctt atctatgaaa tggccgctgg 901 ctacccgcgc ttcttcgcag accagcccat ccagatctat gagaagatcg tctctggaa 961 ggtgcgttc cttcccaact tcagctctga ttgaaggac ctgcgtcgaa acctcctgca 1021 ggtagatctc accaagcgct ttggaaacct caagaatggg gtcaacgata tcaagaacca 1081 caagtggttt gccacaactg actggattgc catctaccag aggaagggtgg aagctccctt 1141 cataccaaag tttaaaggcc ctggggatac gagtaactt gacgactatg aggaagaaga 1201 aatccgggtc tccatcatgc agaagtgtgg caaggagtt tctgagttt aggggcatgc 1261 ctgtcccccc atgggttttc tttttttttt tttttttttt ttggcgcccc 1321 gttggattga acagccagag ggccccagag ttccctgcac ctaatttcac cccacccca 1381 ccctccaggg ttagggggag caggaagccc agataatcag agggacagaa acaccagctg 1441 ctccccctca tccatcatgc cttcccttcac cttccctgc cttcccccac tttcccttc 1501 acagcccccc agcccccctcag ccctcccaagc ccacttctgc ctgtttaaa cgagtttctc 1561 aactccagtc agaccaggta ttgtgggtgt atccaggac agggatggaa aagagggct 1621 cacgtttaac tccagcccccc acccacaccc ccacccaccc caaccacagg cccacttgc 1681 taagggcaaa tgaacgaagc gccaacccctc ctttcggagt aatccctgcct gggaaaggaga 1741 gattttttagt gacatgttca gtgggttgc tgctagaatt tttttaaaaa aacaacaatt 1801 taaaatctta tttaagttcc accagtgcct ccctccctcc ttccctctact cccacccctc 1861 ccatgtcccc ccattccatca aatccatccc aaagagaagc agactgactt tggaaaggaa 1921 ggcgtgggg tttgaacctc cccgtgtcta atcccccgc ggcgcctccc cggggatcc 1981 tctctgccaa tcctgcgagg gtctaggccc ctttaggaag cttccgcctt cttttcccc 2041 aacagacactg tcttcaccct tgggtttga aagccagacca aagcagctgc ccctctccct 2101 gccaaagagg agtcatcccc caaaaagaca gagggggagc cccaaagccca agtcttccct 2161 cccagcagcg tttcccccactccttaat tttattctcc gctagatttt aacgtccagc 2221 cttccctcag ctgagtgggg agggcatccc tgaaaaagg aacagaagag gccaagtc 2281 cccaaagccac ggcgggggt tcaaggctcg agctgctgg gaggggctgc ctgtttact 2341 caccacccag cttccgcctc ccccatcccg ggcgcctccc ctccagctt gctgtcagct 2401 gtccatcacc tctcccccac tttctcatcc tttttttttt ctctcgtaat agaaaagtgg 2461 ggagccgtcg gggagccacc ccattccatcc ccgtatcc ccctctcata acttctcccc 2521 atcccaggag gagttctcag gcctgggtgt gggcccccggg tgggtgcggg ggcgatcaa 2581 cctgtgtct gcaaggacg agacttccctc ttgaacagtg tgctgttgc aacatatttg 2641 aaaactattt ccaataaaagt tttgtttaaa aaaaaaaaaaaa aaaaa

Figure 20b

MGNAAAAGKGSQECSVKEFLAKAKEDFLKKWESPAQNTAHLDQF
ERIKTLGTGSFGRVMLVKHKETGNHYAMKILDKQKVVKLKQIEHTLNEKRIILQAVNFP
FLVKLEFSFKDNNSLYMVEYVPGEMFSHLRRIGRFSEPHARFYAAQIVLTFEYLHS
LDLIVRDLKPNLLIDQQGYIQVTDFGFAKRVKGRTWLCGTPYLAPEIILSKGYNK
AVDWWALGVLIYEMAAGYPPFFADQPIQIYEKIVSGVKRFPSSHFSSDLKDLLRNLLQV
DLTKRFGNLKNGVNDIKNHKFATTDWIAIYQRKVEAPFIPKFKPGPDTSNFDDYEEE
EIRVSINEKCGKEFSEF

PP1 alpha DNA

Figure 21a

ATGTCCGACAGCGAGAAGCTCAACCTGGACTCGATCATGGGCGCCTGCT
GGAAGTGCAGGGCTCGCGGCCTGGCAAGAATGTACAGCTGACAGAGAAC
GAGATCCCGGGTCTGCGCTGAAATCCCGGGAGATTTCTGAGCCAGCC
CATTCTCTGGAGCTGGAGGCACCCCTCAAGATCTGCGGTGACATACACG
GCCAGTACTACGACCTCTGCGACTATTGAGTATGGCGGTTCCCTCCCG
AGAGCAACTACCTCTTCTGGGGACTATGTGGACAGGGCAAGCAGTCC
TTGGAGACCCTGCGCTGCTGGCTATAAGATCAAGTACCCCGAGAA
CTTCTCCTGCTCCGTGGAACCAACCGAGTGTGCCAGCATCAACCGCATCTA
TGGTTCTACGATGAGTGCAAGAGACGCTACAACATCAAACATGTGGAAAA
CCTTCACTGACTGCTCAACTGCCTGCCATCGCGGCCATAGTGGACGAA
AAGATCTTCTGCTGCCACGGAGGCCTGTCCCCGGACCTGCAGTCTATGGA
GCAGATTGGCGGATCATGCGGCCACAGATGTGCCTGACCAGGGCCTGC
TGTGTGACCTGCTGTGGTCTGACCCCTGACAAGGACGTGCAGGGCTGGGGC
GAGAACGACCGTGGCGTCTCTTACCTTGAGCCGAGGTGGTGGCCAA
GTTCCCTCCACAAGCACGACTGGACCTCATGCCGAGCACACCAAGGTGG
TAGAACGACGGCTACGAGTTCTTGCCAAGCGGCAGCTGGTACACTTTC
TCAGCTCCCAACTACTGTGGCGAGTTGACAATGCTGGGCCATGATGAG
TGTGGACGAGACCCCTATGTGCTCTTCCAGATCCTCAAGCCCGCCGACA
AGAACAAAGGGGAAGTACGGCAGTCAGTGGCCTGAACCCCTGGAGGCCG
ACCCATCACCCACCCGCAATTCCGCCAAAGCCAAGAAATAG

Figure 21b

MSDSEKLNLDIIGRLLEVQGSRPGKVNQLTENEIRGLCLKSREIFLSQPILLEL
EAPLKICGDIHGQYYDLLRLFEYGGFPPESNYFLGDYVDRGKQSLETICLLL
AYKIKYPENFFLRLGNHECASINRIYGFYDECKRRYNIKLWKTFTDCNCLPIA
AIVDEKIFCCHGGLSPDLQSMEQIRRIMRPTDVPDQGLLCDLLWSDPDKDVQ
GWGENDRGVSFTFGAEVVAKFLHKHDLDLICRAHQVVEDGYEFFAKRQLVT
LFSAPNYCGEFDNAGAMMSVDELMCSFQILKPADKNKGKYGQFSGLNPGG
RPITPPRNSAKAKK-

Effect of H-ras RNAi and K-ras RNAi on apoptosis

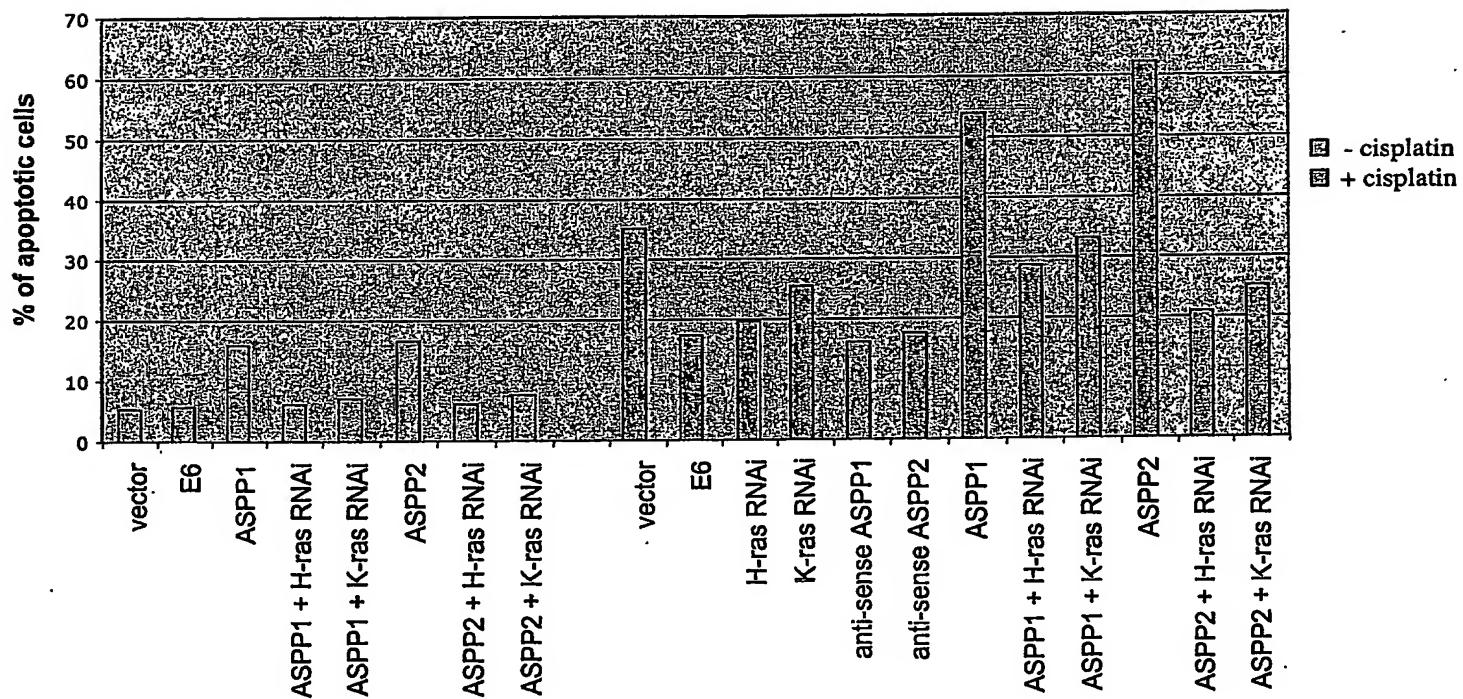


Figure 22

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